



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 166505

**TO: Franco M Salvoza**  
**Location: REM/3B49/3C18**  
**Art Unit: 1648**  
**Friday, September 23, 2005**

**Case Serial Number: 10/654737**

**From: Paul Schulwitz**  
**Location: Biotech-Chem Library**  
**REM-1A65**  
**Phone: 571-272-2527**

**Paul.schulwitz@uspto.gov**

### Search Notes

Examiner Salvoza,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
REM-1A65  
571-272-2527



STIC-Biotech/ChemLib

166-505

From: Page, Thurman  
Sent: Wednesday, September 21, 2005 4:08 PM  
To: STIC-Biotech/ChemLib; Salvoza, Franco  
Cc: Page, Thurman  
Subject: FW: rush sequence search request

Importance: High

RUSH SEARCH APPROVED

-----Original Message-----

From: Salvoza, Franco  
Sent: Wednesday, September 21, 2005 3:59 PM  
To: Page, Thurman  
Subject: rush sequence search request

Mr. Page,  
I'd like to kindly request a rush sequence search for application 10/654,737. It is an overdue amendment which was transferred to me (a new junior examiner) from an examiner that has since left the USPTO.

I am interested in an updated search for SEQ ID NOs: 5 and 6 for this application as well as an interference search to prepare it for allowance.

thank you for your time and consideration.

best regards,

Franco Salvoza

Examiner Franco Salvoza  
AU1648  
REM 3B49  
x8410

RECEIVED  
SEP 21 2005  
STIC/BIOTECH, DIVISION  
(STIC)

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: 9/23  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:28:42 ; Search time 156.61 Seconds  
(without alignments)  
568.004 Million cell updates/sec

Title: US-10-654-737-5

Perfect score: 1172

Sequence: 1 MDPNTVSSFQVDCFLVHRK.....RPPLTPKQKRWARTIRSEV 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1140	97.3	237	5 AAE23116	Aae23116 Influenza
2	1107	94.5	230	8 ADO14171	Ado14171 Influenza
3	1079	92.1	230	8 ADO14175	Ado14175 Influenza
4	1078	92.0	217	8 ADO14178	Ado14178 Influenza
5	1075	91.7	237	5 ABB05772	Abb05772 Influenza
6	1057	90.2	227	8 ADO14179	Ado14179 Influenza
7	1054	89.9	230	2 AA003522	Aa003522 Non-struct
8	1052	89.8	230	4 AA009027	Aae09027 Equine in
9	1050	89.6	227	8 AAE09029	Aae09029 Equine in
10	1050	89.6	227	8 ADO14177	Ado14177 Influenza
11	1047	89.3	230	8 ADO14174	Ado14174 Influenza
12	1046	89.2	227	8 ADO14180	Ado14180 Influenza
13	1035	88.3	230	8 ADO14176	Ado14176 Influenza
14	1021	87.1	230	8 ADO14183	Ado14183 Influenza
15	1006	85.8	202	8 ADO14184	Ado14184 Influenza
16	844	72.0	230	8 ADO14181	Ado14181 Influenza
17	835	71.2	230	8 ADO14172	Ado14172 Influenza
18	813	69.4	173	8 ADO14173	Ado14173 Influenza
19	424	36.2	97	4 AA009028	Aae09028 Equine in
20	415.5	35.5	246	2 AA012714	Aaw12714 Flu NS1-H
21	412	35.2	344	4 ABB071886	Abu71886 Human pro
22	411	35.1	124	8 ADO14182	Ado14182 Influenza
23	407.5	34.8	231	2 AAR20301	Aar20301 Val(1) to
24	406.5	34.7	309	2 AAR13175	Aar13175 NS1 81-RL
25	406.5	34.7	319	2 AAR07945	Aar07945 NS181RLFA

26	406.5	34.7	319	2 AAR13176	Aar13176 NS1 81-RL
27	406.5	34.7	327	2 AAR13177	Aar13177 NS1 81-RL
28	406.5	34.7	335	2 AAR13178	Aar13178 NS1 81 (NA
29	406	34.6	312	4 AAY72521	Aay72521 NS1-P703P
30	406	34.6	312	5 AAU74767	Aau74767 Amino aci
31	406	34.6	312	5 AAU74928	Aau74928 Amino aci
32	405.5	34.6	306	2 AAR38867	Aar38867 Sequence
33	405.5	34.6	306	2 AAR60194	Aar60194 Immunogen
34	405	34.6	262	3 AAB26326	Aab26326 CASB618 p
35	404	34.5	312	4 AAY72522	Aay72522 NS1-P703P
36	404	34.5	312	5 AAU74768	Aau74768 Amino aci
37	404	34.5	312	5 AAU74929	Aau74929 Amino aci
38	403.5	34.4	304	2 AAR60197	Aar60197 Immunogen
39	403.5	34.4	304	2 AAR60207	Aar60207 Immunogen
40	403.5	34.4	335	2 AAR13179	Aar13179 NS1 81 (NV
41	402.5	34.3	150	2 AAW35281	Aaw35281 PorCine s
42	402.5	34.3	150	5 AAE16491	Aae16491 Influenza
43	402.5	34.3	230	2 AAR38868	Aar38868 Sequence
44	402.5	34.3	230	2 AAR60195	Aar60195 Immunogen
45	402.5	34.3	230	2 AAR60226	Aar60226 Immunogen

## ALIGNMENTS

### RESULT 1

AAE23116

ID AAE23116 standard; protein; 237 AA.

XX AC AAE23116;

XX DT 21-AUG-2002 (first entry)

XX DE Influenza A virus/singapore/1/57/ca NS1 mutant protein.

XX KW Attenuated influenza vaccine; prophylactic; therapeutic; infection;

XX OS virucide; mutant; mutein; NS1 protein.

XX OS Influenza A virus.

XX OS Synthetic.

XX PN WO200224876-A2.

XX PD 28-MAR-2002.

XX PF 25-SEP-2001; 2001WO-EP011087.

XX PR 25-SEP-2000; 2000EP-00120896.

XX FA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX PI Katinger H, Egorov A, Ferko B, Romanova J, Katinger D;

XX DR WPI; 2002-416282/44.

XX DR N-PSDB; AAD37061.

XX PT Manufacturing live vaccine, by infecting Vero cells with virus, combining

XX PT cells with serum-free cell culture medium, incubating cells in presence

XX PT of protease and nuclease, harvesting virus and preparing vaccine.

XX PS Example 4; Page 62-63; 90pp; English.

XX CC The present invention relates to a method for isolating viruses from

XX CC various sources and for producing live attenuated influenza vaccines in a

XX CC serum-free African Green monkey kidney (Vero) cell culture under

XX CC conditions where alterations in the surface antigens of the virus due to

XX CC adaptive selection are minimised or prevented. The method is useful for

XX CC the manufacture of whole-virus vaccine, preferably attenuated live

XX CC vaccine. It is useful for prophylactic or therapeutic administration

XX CC against viral infection, preferably influenza virus infections. The

XX CC present sequence is Influenza A virus/singapore/1/57/ca (cold adapted)

XX CC NS1 mutant protein. This sequence is used in the exemplification of the

XX CC invention

XX SQ Sequence 237 AA;  
 Query Match 97.3%; Score 1140; DB 5; Length 237;  
 Best Local Similarity 96.1%; Pred. No. 1.2e-118;  
 Matches 221; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MDPNTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRRDQKSLRGSGTLGLNIETATRA 60  
 DB 1 MDPNTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRRDQKSLRGSGTLGLNIETATRV 60  
 QY 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMD 120  
 DB 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMD 120  
 QY 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
 DB 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
 QY 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230  
 DB 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSKV 230  
 RESULT 2  
 ID ADO14171 standard; protein; 230 AA.  
 AC ADO14171;  
 XX 12-AUG-2004 (first entry)  
 DT Influenza A virus non-structural protein (NS)-1 #1.  
 DE Influenza A virus; A/Udorn/307/73 (H3N2).  
 XX WO2004043404-A2.  
 PN 27-MAY-2004.  
 PD 13-NOV-2003; 2003WO-US036292.  
 PP 13-NOV-2002; 2002US-0425661P.  
 PR 10-JUN-2003; 2003US-0477453P.  
 XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 PA Montelione GT, Krug RM;  
 PI WPI; 2004-420083/39.  
 DR Identifying agents useful for treating influenza virus infection  
 PT comprises identifying compounds that inhibit binding between influenza  
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
 the protein.  
 XX Disclosure; Page 11; 92pp; English.  
 XX This invention relates to a novel method of identifying an inhibitor of  
 CC influenza virus which comprises testing candidate compounds for their  
 CC ability to reduce the extent of binding between influenza virus non-  
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
 CC domain and a dsRNA that binds the protein. The invention may be useful  
 CC for the production of compounds with a virucide activity acting as  
 CC inhibitors of binding between influenza virus non-structural protein-1  
 CC (NS1) and double-stranded RNA. It is possible that binding of double-  
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA

CC -activated protein kinase to remain in an inactive state so that it does  
 CC not catalyse the phosphorylation of translation inhibition factor  
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
 CC replication. The invention is useful as a (high throughput) screening  
 CC method for identifying compounds having inhibitory activity against  
 CC influenza virus. Compounds identified are useful in treating animals,  
 CC including human infected with influenza virus. The present sequence is  
 CC that of an influenza virus non-structural (NS)-1 protein which is related  
 CC to the method of the invention.  
 XX SQ Sequence 230 AA;  
 Query Match 94.5%; Score 1107; DB 8; Length 230;  
 Best Local Similarity 93.5%; Pred. No. 5.9e-115;  
 Matches 215; Conservative 10; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 MDPNTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRRDQKSLRGSGTLGLNIETATRA 60  
 DB 1 MDPNTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRRDQKSLRGSGTLGLDIETATRA 60  
 QY 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMD 120  
 DB 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMD 120  
 QY 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
 DB 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTAEDVKNAGV 180  
 QY 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230  
 DB 181 LIGGLEWNNNTVRVSETLQRFARWSSNENGRPPLTPKQKRWAGTIRSEV 230  
 RESULT 3  
 ID ADO14175 standard; protein; 230 AA.  
 AC ADO14175;  
 XX 12-AUG-2004 (first entry)  
 DT Influenza A virus non-structural protein (NS)-1 #5.  
 DE Influenza A virus; non-structural protein-1; NS1;  
 XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
 KW double-stranded RNA; dsRNA; binding domain; virucide;  
 KW double-stranded-RNA-activated protein kinase; phosphorylation;  
 KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
 KW viral protein replication; screening method; infection.  
 XX Influenza A virus.  
 OS WO2004043404-A2.  
 XX 27-MAY-2004.  
 PD 13-NOV-2003; 2003WO-US036292.  
 PP 13-NOV-2002; 2002US-0425661P.  
 PR 10-JUN-2003; 2003US-0477453P.  
 XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 PA Montelione GT, Krug RM;  
 PI WPI; 2004-420083/39.  
 DR Identifying agents useful for treating influenza virus infection  
 PT comprises identifying compounds that inhibit binding between influenza  
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
 the protein.  
 XX Disclosure; Page 12; 92pp; English.  
 XX





XX Influenza virus; A/equine 1/Suffolk 89.  
 OS BP726316-A2.  
 XX PN  
 XX PD  
 XX 14-AUG-1996.  
 XX 31-JAN-1996; 96EP-00300681.  
 XX 09-FEB-1995; 95GB-00002489.  
 XX (ANIM-) ANIMAL HEALTH TRUST.  
 XX PA  
 XX BI  
 XX Binns M, Birch-Machin I;  
 XX WPI; 1996-364394/37.  
 DR N-PSDB; AAT37435.  
 XX Recombinant equine influenza virus NS1 protein - useful for diagnosis of  
 PT equine influenza A.  
 XX Example; Fig 1A; 20pp; English.  
 XX This sequence represents non-structural protein NS1 of influenza virus  
 CC A/equine 2/Suffolk 89. The NS1 protein is useful for diagnosis of equine  
 CC influenza A infections by detection of anti-NS1 antibodies. The NS1  
 CC coding sequence was isolated using the primer sequences given in AAT37436  
 CC -40. (Updated on 16-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 230 AA;  
 Query Match 89.94; Score 1054; DB 2; Length 230;  
 Best Local Similarity 88.3%; Pred. No. 5e-109;  
 Matches 203; Conservative 15; Mismatches 12; Indels 0; Gaps 0;  
 Qy 1 MDPNTVSSFOVDCFLMHWVRKRVADQELGDAPFLDLRRDQKSLGRGSLGLNLTETAIRA 60  
 Db 1 MDSNTVSSFOVDCFLMHWVRKRVADQELGDAPFLDLRRDQKSLGRGSLGLDLETATRA 60  
 Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMD 120  
 Db 61 GKQIVEQILEESDEAEAFMTIASVPASRYLTDMTLDEMSTRDWFMLMPKQKVAGPLCIRMD 120  
 Qy 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHNTNEDIKNAIGV 180  
 Db 121 QAIMDKNIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHNTNEDVKNAIGV 180  
 Qy 181 LIGGLENNNTVRVSKTLOREAWSSNENGRPPLTPKQKRMARTISEV 230  
 Db 181 LIGGLKNDNTVRVSETLQRFARWSSHENGSRPFPKQKRMERTIEPEV 230  
 RESULT 8  
 AAE09027  
 ID AAE09027 standard; protein; 230 AA.  
 AC AAE09027;  
 XX  
 XX 15-NOV-2001 (first entry)  
 XX  
 XX Equine influenza virus H3N8 Peiwt1NS230 protein.  
 XX  
 XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;  
 XX vaccine; neiwt1NS891 DNA; Peiwt1NS230 protein.  
 XX  
 XX Equine influenza virus H3N8.  
 XX WO200160849-A2.  
 XX  
 XX 23-AUG-2001.  
 XX  
 XX 16-FEB-2001; 2001WO-US005048.  
 XX  
 XX

PR 16-FEB-2000; 2000US-00506286.  
 XX (UYPI-) UNIV PITTSBURGH.  
 XX Dowling PW, Youngner JS;  
 XX WPI; 2001-522584/57.  
 DR N-PSDB; AAD15678.  
 XX Novel isolated equine influenza virus (wild-type and cold-adapted)  
 PT proteins and viruses containing nucleic acid molecules encoding the  
 PT proteins, which are useful for protecting animals from influenza virus  
 PT infections.  
 XX  
 XX Claim 5; Page 72-73; 172pp; English.  
 XX  
 XX The patent discloses cold-adapted equine influenza viruses and  
 CC reassortant influenza A viruses comprising at least one genome segment of  
 CC such an equine influenza virus, wherein the equine influenza virus genome  
 CC segment confers at least one identifying phenotype of the cold-adapted  
 CC equine influenza virus, such as cold adaptation, temperature sensitivity,  
 CC dominant interference or attenuation. The viruses are useful for  
 CC protecting animals from diseases caused by influenza viruses. They are  
 CC also used as vaccines. The present sequence is an equine influenza (ei)  
 CC virus H3N8 Peiwt1 (wild type) NS230 protein which is encoded by  
 CC neiwt1NS891 DNA  
 XX  
 SQ Sequence 230 AA;  
 Query Match 89.8%; Score 1052; DB 4; Length 230;  
 Best Local Similarity 87.8%; Pred. No. 8.4e-109;  
 Matches 202; Conservative 16; Mismatches 12; Indels 0; Gaps 0;  
 Qy 1 MDPNTVSSFOVDCFLMHWVRKRVADQELGDAPFLDLRRDQKSLGRGSLGLNLTETAIRA 60  
 Db 1 MDSNTVSSFOVDCFLMHWVRKRVADQELGDAPFLDLRRDQKSLGRGSLGLDLETATRA 60  
 Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMD 120  
 Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSTRDWFMLMPKQKVAGPLCIRMD 120  
 Qy 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHNTNEDIKNAIGV 180  
 Db 121 QAIMDKNIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHNTNEDVKNAIGV 180  
 Qy 181 LIGGLENNNTVRVSKTLOREAWSSNENGRPPLTPKQKRMARTISEV 230  
 Db 181 LIGGLKNDNTVRVSETLQRFARWSSHENGSRPFPKQKRMERTIEPEV 230  
 RESULT 9  
 AAE09029  
 ID AAE09029 standard; protein; 230 AA.  
 XX  
 XX AAE09029;  
 XX  
 XX 15-NOV-2001 (first entry)  
 XX  
 XX Equine influenza virus H3N8 Peiwt1NS230 protein.  
 XX  
 XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;  
 XX vaccine; neiwt1NS891 DNA; Peiwt1NS230 protein.  
 XX  
 XX Equine influenza virus H3N8.  
 XX WO200160849-A2.  
 XX  
 XX 23-AUG-2001.  
 XX  
 XX 16-FEB-2001; 2001WO-US005048.  
 XX  
 XX 16-FEB-2000; 2000US-00506286.  
 XX

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PA (UYFI-) UNIV PITTSBURGH.
PI Dowling PW, Youngner JS;
XX
XX
XX WPI; 2001-522584/57.
XX N-PSDB; AAD15681.
XX
XX Novel isolated equine influenza virus (wild-type and cold-adapted)
XX proteins and viruses containing nucleic acid molecules encoding the
XX PT proteins, which are useful for protecting animals from influenza virus
XX PT infections.
XX
XX PS Claim 5; Page 77; 172pp; English.
XX
XX The patent discloses cold-adapted equine influenza viruses and
XX CC reassortant influenza A viruses comprising at least one genome segment of
XX CC such an equine influenza virus, wherein the equine influenza virus genome
XX CC segment confers at least one identifying phenotype of the cold-adapted
XX CC equine influenza virus, such as cold adaptation, temperature sensitivity,
XX CC dominant interference or attenuation. The viruses are useful for
XX CC protecting animals from diseases caused by influenza viruses. They are
XX CC also used as vaccines. The present sequence is equine influenza (ei)
XX CC virus H3N8 Peical (cold adapted) NS230 protein which is encoded by
XX CC neicalNS988 DNA
XX
XX SQ Sequence 230 AA;
XX
XX Query Match 89.8%; Score 1052; DB 4; Length 230;
XX Best Local Similarity 87.8%; Pred. No. 8.4e-109;
XX Matches 202; Conservative 16; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 1 MDNTVSSFQVDCFLMHWKRVADQELGDPFLDLRRDQKSLRGSTGLGNIETATRA 60
XX DB 1 MDSNTVSSFQVDCFLMHWKRVADQELGDPFLDLRRDQKSLRGSTGLGDIETATRA 60
XX
XX QY 61 GKQIVRIKESDEALKMTIASPASRYLTDMTIEMSRDWFMMPKQKVGAGLCIRMD 120
XX DB 61 GKQIVEQILEESDEALKMTIASPASRYLTDMTIEMSRDWFMMPKQKVTGSLCIRMD 120
XX
XX QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
XX DB 121 QAIMDKMIILKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAGV 180
XX
XX QY 181 LIGGLENNNTVRVSKTQRFAMRSSNENGRPPLTPKQKRMARTIRSEV 230
XX DB 181 LIGGLKNDNTVRISLQRFAMRSSHENGSRPSPKQKRMWERTISPEV 230
XX
XX RESULT 10
XX ID ADO14177 standard; protein; 227 AA.
XX
XX AC ADO14177;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE Influenza A virus non-structural protein (NS)-1 #7.
XX
XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;
XX KW double-stranded RNA; dSRNA; binding domain; virucide;
XX KW double-stranded-RNA-activated protein kinase; phosphorylation;
XX KW translation inhibition factor; eIF2alpha; viral protein synthesis;
XX KW viral protein replication; screening method; infection.
XX
XX OS Influenza A virus.
XX
XX PN WO2004043404-A2.
XX
XX PD 27-MAY-2004.
XX
XX PF 13-NOV-2003; 2003WO-US036292.
XX
XX PR 13-NOV-2002; 2002US-0425661P.
XX
PR 10-JUN-2003; 2003US-0477453P.
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX PI Montelione GT, Krug RM;
XX
XX WPI; 2004-420083/39.
XX
XX Identifying agents useful for treating influenza virus infection
XX PT comprises identifying compounds that inhibit binding between influenza
XX PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
XX PT the protein.
XX
XX PS Disclosure; Page 13; 92pp; English.
XX
XX This invention relates to a novel method of identifying an inhibitor of
XX CC influenza virus which comprises testing candidate compounds for their
XX CC ability to reduce the extent of binding between influenza virus non-
XX CC structural protein-1 (NS1) or its double-stranded RNA (dSRNA) binding
XX CC domain and a dSRNA that binds the protein. The invention may be useful
XX CC for the production of compounds with a virucide activity acting as
XX CC inhibitors of binding between influenza virus non-structural protein-1
XX CC (NS1) and double-stranded RNA. It is possible that binding of double-
XX CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
XX CC -activated protein kinase to remain in an inactive state so that it does
XX CC not catalyze the phosphorylation of translation inhibition factor
XX CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
XX CC replication. The invention is useful as a (high throughput) screening
XX CC method for identifying compounds having inhibitory activity against
XX CC influenza virus. Compounds identified are useful in treating animals,
XX CC including human infected with influenza virus. The present sequence is
XX CC that of an influenza virus non-structural (NS)-1 protein which is related
XX CC to the method of the invention.
XX
XX SQ Sequence 227 AA;
XX
XX Query Match 89.6%; Score 1050; DB 8; Length 227;
XX Best Local Similarity 91.2%; Pred. No. 1.4e-108;
XX Matches 207; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 4 NTVSSFQVDCFLMHWKRVADQELGDPFLDLRRDQKSLRGSTGLGNIETATRA 63
XX DB 1 NTVSSFQVDCFLMHWKRVADQELGDPFLDLRRDQKSLRGSTGLGDIETATRA 60
XX
XX QY 64 IVERILKEESDEALKMTIASPASRYLTDMTIEMSRDWFMMPKQKVGAGLCIRMDQAI 123
XX DB 61 IVERILVEESDEALKMTIVSMPASRYLTDMTIEMSRDWFMMPKQKVGAGLCIRMDQAI 120
XX
XX QY 124 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 183
XX DB 121 MDKNIILKANFSVISRLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAGIDLIG 180
XX
XX QY 184 GLEWNNNTVRVSKTQRFAMRSSNENGRPPLTPKQKRMARTIRSEV 230
XX DB 181 GLEWNDNTVRVSETLQRFAMRSSNEDGRPLLPKQKRMARTIESEV 227
XX
XX RESULT 11
XX ID ADO14174 standard; protein; 230 AA.
XX
XX AC ADO14174;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE Influenza A virus non-structural protein (NS)-1 #4.
XX
XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;
XX KW double-stranded RNA; dSRNA; binding domain; virucide;
XX KW double-stranded-RNA-activated protein kinase; phosphorylation;
XX KW translation inhibition factor; eIF2alpha; viral protein synthesis;
XX KW viral protein replication; screening method; infection.
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XX XX

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XX Influenza A virus.  
 PN WO2004043404-A2.  
 XX 27-MAY-2004.  
 XX 13-NOV-2003; 2003WO-US036292.  
 XX 13-NOV-2003; 2002US-0425661P.  
 PR 10-JUN-2003; 2003US-0477453P.  
 XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 PA Montellione GT, Krug RM;  
 PI WPI; 2004-420083/39.  
 XX Identifying agents useful for treating influenza virus infection  
 PT comprises identifying compounds that inhibit binding between influenza  
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
 PT the protein.  
 XX Disclosure; Page 12; 92pp; English.  
 PS This invention relates to a novel method of identifying an inhibitor of  
 CC influenza virus which comprises testing candidate compounds for their  
 CC ability to reduce the extent of binding between influenza virus non-  
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
 CC domain and a dsRNA that binds the protein. The invention may be useful  
 CC for the production of compounds with a virucide activity acting as  
 CC inhibitors of binding between influenza virus non-structural protein-1  
 CC (NS1) and double-stranded RNA. It is possible that binding of double-  
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
 CC activated protein kinase to remain in an inactive state so that it does  
 CC not catalyze the phosphorylation of translation inhibition factor  
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
 CC replication. The invention is useful as a (high throughput) screening  
 CC method for identifying compounds having inhibitory activity against  
 CC influenza virus. Compounds identified are useful in treating animals,  
 CC including human infected with influenza virus. The present sequence is  
 CC that of an influenza virus non-structural (NS)-1 protein which is related  
 CC to the method of the invention.  
 XX Sequence 230 AA;  
 SQ  
 Query Match 89.3%; Score 1047; DB 8; Length 230;  
 Best Local Similarity 88.7%; Pred. No. 3e-108;  
 Matches 204; Conservative 13; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 MDPNTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRQKSLRGSGTLGNIETATRA 60  
 DB 1 MDSNTVSSFOVDCFLHVRKRVADQEMGDAPFLDLRLRQKSLRGSGTLGDIETATRA 60  
 QY 61 GKQIVERILKEESDEALKYMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGSLCIRMD 120  
 DB 61 GKQIVERILEESDEALKYMTIASAPVSRYPDMLTEMSRDWFMMPKQKVGSLCIRMD 120  
 QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSLPGHTNEDIKNATGV 180  
 DB 121 QAIMDKNITLKANFSIIIFDRLETLILLRAFTTEGAIVGEISVPVSLPGHTDEDVKNATGV 180  
 QY 181 LIGGLEWNNNTVRSKTLQRPFAWRSSNENGRPPLTPKQKRWARTIRSEV 230  
 DB 181 LIGGLEWNNNTVRSKTLQRPFAWRSSNENRRPPLTPKQKRWARTIRSEV 230  
 RESULT 12  
 ID ADO14180  
 ID ADO14180 standard; protein; 227 AA.  
 XX ADO14180;  
 AC  
 XX 12-AUG-2004 (first entry)  
 DT

XX Influenza A virus non-structural protein (NS)-1 #10.  
 DE influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
 XX double-stranded RNA; dsRNA; binding domain; virucide;  
 KW double-stranded-RNA-activated protein kinase; phosphorylation;  
 KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
 KW viral protein replication; screening method; infection.  
 XX Influenza A virus.  
 OS WO2004043404-A2.  
 XX 27-MAY-2004.  
 XX 13-NOV-2003; 2003WO-US036292.  
 XX 13-NOV-2003; 2002US-0425661P.  
 PR 10-JUN-2003; 2003US-0477453P.  
 XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 PA Montellione GT, Krug RM;  
 PI WPI; 2004-420083/39.  
 XX Identifying agents useful for treating influenza virus infection  
 PT comprises identifying compounds that inhibit binding between influenza  
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
 PT the protein.  
 XX Disclosure; Page 13-14; 92pp; English.  
 PS This invention relates to a novel method of identifying an inhibitor of  
 CC influenza virus which comprises testing candidate compounds for their  
 CC ability to reduce the extent of binding between influenza virus non-  
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
 CC domain and a dsRNA that binds the protein. The invention may be useful  
 CC for the production of compounds with a virucide activity acting as  
 CC inhibitors of binding between influenza virus non-structural protein-1  
 CC (NS1) and double-stranded RNA. It is possible that binding of double-  
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
 CC activated protein kinase to remain in an inactive state so that it does  
 CC not catalyze the phosphorylation of translation inhibition factor  
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
 CC replication. The invention is useful as a (high throughput) screening  
 CC method for identifying compounds having inhibitory activity against  
 CC influenza virus. Compounds identified are useful in treating animals,  
 CC including human infected with influenza virus. The present sequence is  
 CC that of an influenza virus non-structural (NS)-1 protein which is related  
 CC to the method of the invention.  
 XX Sequence 227 AA;  
 SQ  
 Query Match 89.2%; Score 1046; DB 8; Length 227;  
 Best Local Similarity 90.7%; Pred. No. 3.9e-108;  
 Matches 206; Conservative 8; Mismatches 13; Indels 0; Gaps 0;  
 QY 4 NTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRQKSLRGSGTLGNIETATRAKQ 63  
 DB 1 NTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRQKSLRGSGTLGDIETATRAKQ 60  
 QY 64 IVERILKEESDEALKYMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGSLCIRMDQAI 123  
 DB 61 IVERILEESDETLKMTIASAPAFRYPTDMLTEMSRDWFMMPKQKVGSLCIRMDQAI 120  
 QY 124 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSLPGHTNEDIKNATGV 183  
 DB 121 MDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSLPGHTNEDVKNATGV 180  
 QY 184 GLEWNNNTVRSKTLQRPFAWRSSNENGRPPLTPKQKRWARTIRSEV 230  
 DB 181 GLEWNNNTVRSKTLQRPFAWRSSNENGRPPLTPKQKRWARTIRSEV 227

**RESULT 13**

AD014176

ID ADO14176 standard; protein; 230 AA.

XX

AC ADO14176:

2000

DT 12-AUG-2004 (first entry)

DE Influenza A virus non-structural protein (NS)-1 #6.  
DX  
XX  
XX Influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
XX double-stranded RNA; dsRNA; binding domain; virucide;  
KW double-stranded RNA-activated protein kinase phosphorylation;  
KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
KW viral protein replication; screening method; infection.

**XX**

**Influenza A virus**

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WO2004043404-A2

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PR 13-NOV-2002; 2002US-0425661P.  
PR 10-JUN-2003; 2003US-0477453P.  
XX  
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.



PI Montelione GT, Krug RM;  
DR WPI; 2004-420083/39.  
XX  
XX Identifying agents useful for treating influenza virus infection  
PT comprises identifying compounds that inhibit binding between influenza  
PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
PT the protein.  
XX  
XX Disclosure; Page 12-13; 92pp; English.  
XX  
XX This invention relates to a novel method of identifying an inhibitor of  
CC influenza virus which comprises testing candidate compounds for their  
CC ability to reduce the extent of binding between influenza virus non-  
CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
CC domain and a dsRNA that binds the protein. The invention may be useful  
CC for the production of compounds with a virucide activity acting as  
CC inhibitors of binding between influenza virus non-structural protein-1  
CC (NS1) and double-stranded RNA. It is possible that binding of double-  
CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
CC -activated protein kinase to remain in an inactive state so that it does  
CC not catalyse the phosphorylation of translation inhibition factor  
CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
CC replication. The invention is useful as a (high throughput) screening  
CC method for identifying compounds having inhibitory activity against  
CC influenza virus. Compounds identified are useful in treating animals,  
CC including human infected with influenza virus. The present sequence is  
CC that of an influenza virus non-structural (NS)-1 protein which is related  
CC to the method of the invention.

Sequence 230 AA:

## De

Overall Match 88.3%. Score 1035. DB 8: Tenath 230:

Query Match 88.3%, Score 1035, SS 9, Length 250,  
Post Recall similarity 88.3%, Pred No 6 7e-107.

BEST LOCAL SIMILARITY 88.3%; FREQ. NO: 6.7E-107;  
Matches 202; Consecutive 13; Mismatches 14;  
Indels 0; Gaps

Matches 203; Conservative 13; Mismatches 14; Errors 0; Gaps

[illegible]

QY I MDPN TVSS FQVDC F LWH VRKR VADQELGDAPFLDURLRRDQNSLRGRGSLGJUNIEIAIRA 80

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61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMD 12

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Best Local Similarity 85.7%; Pred. No. 2.5e-105; Matches 197; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRA 60  
Db 1 MDSNTVSSFOVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETATRE 60

Qy 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWFMLMPKQVAGPLCIRMD 120  
Db 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWFMLMPKQVAGPLCIRMD 120

Qy 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
Db 121 QAVWGKTIILKANFSVIFNRLEALILRAFTDEGAIVGEISPLSPGHTNEDVKNAGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKQWARTIRSEV 230  
Db 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKQWARTIRSEV 230

RESULT 15  
ADO14184  
ID ADO14184 standard; protein; 202 AA.  
XX AC ADO14184;  
XX DT 12-AUG-2004 (first entry)  
XX DE Influenza A virus non-structural protein (NS)-1 #14.  
XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
KW double-stranded RNA; dsRNA; binding domain; virucide;  
KW double-stranded-RNA-activated protein kinase; phosphorylation;  
KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
KW viral protein replication; screening method; infection.  
XX OS Influenza A virus; STRAIN A/FORT MONMOUTH/1/47.  
XX PN WO2004043404-A2.  
XX PD 27-MAY-2004.  
XX PP 13-NOV-2003; 2003WO-US036292.  
XX PR 13-NOV-2003; 2002US-0425661P.  
XX PR 10-JUN-2003; 2003US-0477453P.  
XX PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
XX PI Montelione GT, Krug RM;  
XX DR WPI; 2004-420083/39.  
XX PT Identifying agents useful for treating influenza virus infection  
PT comprises identifying compounds that inhibit binding between influenza  
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PT the protein.  
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XX CC This invention relates to a novel method of identifying an inhibitor of  
CC influenza virus which comprises testing candidate compounds for their  
CC ability to reduce the extent of binding between influenza virus non-  
CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
CC domain and a dsRNA that binds the protein. The invention may be useful  
CC for the production of compounds with a virucide activity acting as  
CC inhibitors of binding between influenza virus non-structural protein-1  
CC (NS1) and double-stranded RNA. It is possible that binding of double-  
CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
CC -activated protein kinase to remain in an inactive state so that it does  
CC not catalyse the phosphorylation of translation inhibition factor  
CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
CC replication. The invention is useful as a (high throughput) screening

CC method for identifying compounds having inhibitory activity against  
CC influenza virus. Compounds identified are useful in treating animals,  
CC including human infected with influenza virus. The present sequence is  
CC that of an influenza virus non-structural (NS)-1 protein which is related  
CC to the method of the invention.

SQ Sequence 202 AA;

Query Match 85.8%; Score 1006; DB 8; Length 202;  
Best Local Similarity 97.5%; Pred. No. 9.8e-104;  
Matches 197; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRA 60  
Db 1 MDPNTVSSFOVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETATRV 60

Qy 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWFMLMPKQVAGPLCIRMD 120  
Db 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWFMLMPKQVAGPLCIRMD 120

Qy 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
Db 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNAGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKQWARTIRSEV 202  
Db 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKQWARTIRSEV 202

Search completed: September 22, 2005, 21:42:21  
Job time : 159.61 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:33:28 ; Search time 32.1083 Seconds  
(without alignments)  
689.226 Million cell updates/sec

Title: US-10-654-737-5

Perfect score: 1172

Sequence: 1 MDPNTVSSFQVDCFLHVRK.....RPPLTPKQKRMARTIRSEV 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:\*

2: pir1:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1142	97.4	237	1 MNIV77	nonstructural prot
2	1140	97.3	237	1 MNIV14	nonstructural prot
3	1128	96.2	237	1 MNIVC1	nonstructural prot
4	1111	94.8	230	1 MNIV1	nonstructural prot
5	1107	94.5	230	2 S09648	nonstructural prot
6	1092	93.2	230	1 MNIVA2	nonstructural prot
7	1079	92.1	230	1 MNIVA3	nonstructural prot
8	1078	92.0	217	1 MNIV61	nonstructural prot
9	1075	91.7	230	1 MNIVA4	nonstructural prot
10	1075	91.7	237	1 MNIV1A	nonstructural prot
11	1061	90.5	227	1 MNIVX3	nonstructural prot
12	1057	90.2	227	1 MNIVX9	nonstructural prot
13	1057	90.2	230	1 MNIV1F	nonstructural prot
14	1055	90.0	230	1 MNIV1A	nonstructural prot
15	1050	89.6	227	1 MNIVX5	nonstructural prot
16	1050	89.6	237	1 MNIV1K	nonstructural prot
17	1049	89.5	227	1 MNIVX7	nonstructural prot
18	1046	89.2	227	1 MNIVX1	nonstructural prot
19	1029	87.8	230	1 D45539	nonstructural prot
20	999	85.2	202	1 MNIV47	nonstructural prot
21	844	72.0	230	1 MNIV16	nonstructural prot
22	840	71.7	230	1 MNIVAS	nonstructural prot
23	840	71.7	230	1 MNIVA6	nonstructural prot
24	838	71.5	230	1 MNIVA8	nonstructural prot
25	837	71.4	230	1 MNIV47	nonstructural prot
26	824	70.3	230	2 A45575	nonstructural prot
27	437	37.3	89	2 B92982	nonstructural prot
28	411	35.1	124	1 MNIV71	nonstructural prot
29	151	12.9	32	2 PQ0419	nonstructural prot

30	133	11.3	32	2 PQ0425	nonstructural prot
31	131	11.2	32	2 PQ0413	nonstructural prot
32	90	7.7	361	2 AB0584	PhoB-like ATP-bind
33	89.5	7.6	838	2 G84599	probable retroelem
34	89	7.6	359	2 E85566	probable ATP-bind
35	89	7.6	359	2 B64801	YbeZ protein - Esc
36	89	7.6	359	2 B90716	probable ATP-bind
37	88	7.5	385	2 AG1835	hypothetical prote
38	88	7.5	436	2 F86486	protein P28J9.3 [1
39	86	7.3	370	2 AG0319	conserved hypothe
40	86	7.3	557	2 A70480	carbamoyl-phosphat
41	84.5	7.2	482	2 E97748	virB10 protein (im
42	84	7.2	189	2 C87605	RNA polymerase sig
43	84	7.2	553	2 F84270	dnak-type molecula
44	84	7.2	769	2 F87486	outer membrane pro
45	83.5	7.1	446	2 T26039	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

MNIV77

nonstructural protein NS1 - influenza A virus (strain A/USSR/90/77 [H1N1])

C:Species: influenza A virus

C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 16-Jul-1999

C:Accession: E92991; A04090

R:Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A:Title: Sequential mutations in the NS genes of influenza virus field strains.

A:Reference number: A92991; MUID:83164298; PMID:6834468

A:Accession: E92991

A:Molecule type: genomic RNA

A:Residues: 1-237 <KRY>

A:Cross-references: GB:K00578; NID:g324839; PTDN:AAA43540.1; PID:g324841

C:Genetics:

A:Map position: segment 8

C:Superfamily: influenza virus nonstructural protein NS1

C:Keywords: alternative splicing

Query Match	97.4%	Score 1142;	DB 1;	Length 237;
Best Local Similarity	97.0%	Pred. No. 3.1e-91;		
Matches	223;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0;
QY	1	MDPNTVSSFQVDCFLHVRKRVADQELGDAPFLDRDRDQKSLRGSTGLNIETATRA	60	
Db	1	MDPNTVSSFQVDCFLHVRKRVADQELGDAPFLDRDRDQKSLRGSTGLNIETATCV	60	
QY	61	GKQIVERILKEESDEALAKMTWASAPASYLTDMTTEEMSRDWMFLMPKQKVGAPLCIRMD	120	
Db	61	GKQIVERILKEESDEALAKMTWASAPASYLTDMTTEEMSRDWMFLMPKQKVGAPLCIRMD	120	
QY	121	QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV	180	
Db	121	QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV	180	
QY	181	LIGGLEWNNVTVRVSKTLQRFAPWSSNENGRPPLTPKQKRMARTIRSEV	230	
Db	181	LIGGLEWNNVTVRVSKTLQRFAPWSSNENGRPPLTPKQKRMARTIRSEV	230	

##### RESULT 2

MNIV14

nonstructural protein NS1 - influenza A virus (strain A/FW/1/50 [H1N1])

C:Species: influenza A virus

C>Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 16-Jul-1999

C:Accession: A92991; A04090; B92982

R:Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A:Title: Sequential mutations in the NS genes of influenza virus field strains.

A:Reference number: A92991; MUID:83164298; PMID:6834468

A:Accession: A92991

A:Molecule type: genomic RNA

181 LIGSEWNDNTVRVSETLORFAWRSSNENGRPDLTPKOREMAGTIRSEV 230

```
RESULT 6
MNIV2
nonstructural protein NS1 - influenza A virus (strain A/mallard/New York/6750/78)
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: G32662
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, a
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: G32662
A:Molecule type: genomic RNA
A:Residues: 1-230 <TR>
A:CROSS-references: UNIPROT:P13138
C:Genetics:
A:Gene: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 93.2%; Score 1092; DB 1; Length 230;
Best Local Similarity 92.6%; Pred. No. 6.2e-87;
Matches 213; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPEFLRLRDQSLRGSGTLGNIETATRA 60
Db 1 MDSNTVSSFOVDCFLHVRKRVADQELGDAPEFLRLRDQSLRGSGTLGDIETATRA 60

Qy 61 GQIVIRILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMD 120
Db 61 GQIVIRILEESDEALKMTIASVPASRYLTDMTTEMSRDWFMMPKQKVGAGSLCIRMD 120

Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTDVEDVNAIGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPLTPPKQKRWARTIESEV 230
Db 181 LIGGLEWNDNTVRVSETLQRFAPWSSNENGRPLTPPKQKRWARTIESEV 230

RESULT 7
MNIV3
nonstructural protein NS1 - influenza A virus (strain A/mallard/New York/6874/78)
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: E32662
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, a
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: E32662
A:Molecule type: genomic RNA
A:Residues: 1-230 <TR>
A:CROSS-references: UNIPROT:P13139
C:Genetics:
A:Gene: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.1%; Score 1079; DB 1; Length 230;
Best Local Similarity 91.7%; Pred. No. 8.2e-86;
Matches 211; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPEFLRLRDQSLRGSGTLGNIETATRA 60
Db 1 MDSNTVSSFOVDCFLHVRKRVADQELGDAPEFLRLRDQSLRGSGTLGDIETATRA 60

Qy 61 GQIVIRILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMD 120
Db 61 GQIVIRILEESDEALKMTIASVPASRYLTDMTTEMSRDWFMMPKQKVGAGSLCIRMD 120
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Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTDVEDVNAIGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPLTPPKQKRWARTIESEV 230
Db 181 LIGGLEWNDNTVRVSETLQRFAPWSSNENGRPLTPPKQKRWARTIESEV 230

RESULT 8
MNIV61
nonstructural protein NS1 - influenza A virus (strain A/Ann Arbor/6/60 [H2N2])
C:Species: influenza A virus
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: G31831
R:Cox, N.J.; Kitame, F.; Kendal, A.P.; Maassab, H.F.; Naeve, C.
Virology 167, 554-567, 1988
A:Title: Identification of sequence changes in the cold-adapted, live attenuated influen:
A:Reference number: A31831; MUID:89073759; PMID:2974219
A:Accession: G31831
A:Molecule type: genomic RNA
A:Residues: 1-217 <CO>
A:CROSS-references: GB:M23968; GB:J04349; GB:M23969; NID:G324860; PIDN:AAA43553.1; PID:9;
C:Genetics:
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.0%; Score 1078; DB 1; Length 217;
Best Local Similarity 96.3%; Pred. No. 9.3e-86;
Matches 209; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPEFLRLRDQSLRGSGTLGNIETATRA 60
Db 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPEFLRLRDQSLRGSGTLGNIETATRV 60

Qy 61 GQIVIRILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMD 120
Db 61 GQIVIRILEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMD 120

Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTDVEDVNAIGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPLTPPK 217
Db 181 LIGGLEWNDNTVRVSKTLQRFAPWSSNENGRPLTPK 217

RESULT 9
MNIV44
nonstructural protein NS1 - influenza A virus (strain A/pintail/Alberta/119/79)
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: G32662
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, a
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: G32662
A:Molecule type: genomic RNA
A:Residues: 1-230 <TR>
A:CROSS-references: UNIPROT:P13140
C:Genetics:
A:Gene: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 91.7%; Score 1075; DB 1; Length 230;
Best Local Similarity 91.3%; Pred. No. 1.8e-85;
Matches 210; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
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Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRA 60  
Db 1 MDSNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRA 60  
Qy 61 GKQIVERILKEESDEALKWMTASAPASRYLTDMTIEEMSRDWFMLMPKQKVGAGPLCIRMD 120  
Db 61 GKQIVERILKEESDEALKWMTASAPASRYLTDMTIEEMSRDWFMLMPKQKVGAGPLCIRMD 120  
Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
Db 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
Qy 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPPLTPKQKRWARTIRSEV 230  
Db 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPPLTPKQKRWARTIRSEV 230  
RESULT 10  
MNIVA  
nonstructural protein NS1 - influenza A virus (strain A/Udm/72 [H3N2])  
C:Species: influenza A virus  
C:Date: 31-Oct-1980 #sequence\_revision 31-Oct-1980 #text\_change 09-Jul-2004  
C:Accession: A04088; S11297  
R:Lamb, R.A.; Lai, C.J.  
Cell 21, 475-485, 1980  
A:Title: Sequence of interrupted and uninterrupted mRNAs and cloned DNA coding for the  
A:Reference number: A90801; MUID:81001890; PMID:7407920  
A:Accession: A04088  
A:Molecule type: mRNA  
A:Residues: 1-237 <NAK>  
A:Cross-references: UNIPROT:P03495; GB:V01102; GB:J02169; NID:660797; PIDN:CAA24288.1; F  
A:Experimental source: strain A/Udm/72 [H3N2]  
R:Robertson, J.S.  
Nucleic Acids Res. 6, 3745-3757, 1979  
A:Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza  
A:Reference number: S11286; MUID:80034428; PMID:493121  
A:Accession: S11297  
A:Molecule type: Genomic RNA  
A:Residues: 1-15 <ROB>  
A:Cross-references: GB:J02118  
A:Experimental source: strain A/Fpv/Rostock/34 [H7N1]  
A:Note: the authors translated the codon CAG for residue 10 as Glu  
C:Genetics:  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing  
Query Match 91.7%; Score 1075; DB 1; Length 237;  
Best Local Similarity 90.4%; Pred. No. 1.9e-85;  
Matches 208; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRA 60  
Db 1 MDSNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRA 60  
Qy 61 GKQIVERILKEESDEALKWMTASAPASRYLTDMTIEEMSRDWFMLMPKQKVGAGPLCIRMD 120  
Db 61 GKQIVERILKEESDEALKWMTASAPASRYLTDMTIEEMSRDWFMLMPKQKVGAGPLCIRMD 120  
Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
Db 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
Qy 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPPLTPKQKRWARTIRSEV 230  
Db 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPPLTPKQKRWARTIRSEV 230  
RESULT 11  
MNIVK3  
nonstructural protein NS1 - influenza A virus (strain A/Duck/England/56 [H1N6]) (fragme  
C:Species: influenza A virus  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999

C:Accession: C27846  
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.  
Virology 158, 465-469, 1987  
A:Title: Genetic divergence of the NS genes of avian influenza viruses.  
A:Reference number: A94361; MUID:87236215; PMID:2954302  
A:Accession: C27846  
A:Molecule type: genomic RNA  
A:Residues: 1-227 <NAK>  
A:Cross-references: GB:M16563; NID:G324786; PIDN:AAA43510.1; PID:G324787  
C:Genetics:  
A:Gene: NS1  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing; nonstructural protein  
Query Match 90.5%; Score 1061; DB 1; Length 227;  
Best Local Similarity 91.2%; Pred. No. 2.9e-84;  
Matches 207; Conservative 11; Mismatches 9; Indels 0; Gaps 0;  
Qy 4 NTVSSFOVDCFLHVRKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRACKQ 63  
Db 1 NTVSSFOVDCFLHVRKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRACKQ 60  
Qy 64 IVERILKEESDEALKWMTASAPASRYLTDMTIEEMSRDWFMLMPKQKVGAGPLCIRMDQAI 123  
Db 61 IVERILKEESDEALKWMTASAPASRYLTDMTIEEMSRDWFMLMPKQKVGAGPLCIRMDQAI 120  
Qy 124 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 183  
Db 121 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 180  
Qy 184 GLEWNNNTVRVSKTLQRFARWSSNENGRPPPLTPKQKRWARTIRSEV 230  
Db 181 GLEWNNNTVRVSKTLQRFARWSSNENGRPPPLTPKQKRWARTIRSEV 227  
RESULT 12  
MNIVX9  
nonstructural protein NS1 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fre  
C:Species: influenza A virus  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
C:Accession: I27846  
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.  
Virology 158, 465-469, 1987  
A:Title: Genetic divergence of the NS genes of avian influenza viruses.  
A:Reference number: A94361; MUID:87236215; PMID:2954302  
A:Accession: I27846  
A:Molecule type: genomic RNA  
A:Residues: 1-227 <NAK>  
A:Cross-references: GB:M17070; NID:G324854; PIDN:AAA43548.1; PID:G324855  
C:Genetics:  
A:Gene: NS1  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing; nonstructural protein  
Query Match 90.2%; Score 1057; DB 1; Length 227;  
Best Local Similarity 90.7%; Pred. No. 6.4e-84;  
Matches 206; Conservative 11; Mismatches 10; Indels 0; Gaps 0;  
Qy 4 NTVSSFOVDCFLHVRKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRACKQ 63  
Db 1 NTVSSFOVDCFLHVRKRVADQELGDAPFLDLRRDQKSLRGSTGLGNIETAIRACKQ 60  
Qy 64 IVERILKEESDEALKWMTASAPASRYLTDMTIEEMSRDWFMLMPKQKVGAGPLCIRMDQAI 123  
Db 61 IVERILKEESDEALKWMTASAPASRYLTDMTIEEMSRDWFMLMPKQKVGAGPLCIRMDQAI 120  
Qy 124 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 183  
Db 121 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 180  
Qy 184 GLEWNNNTVRVSKTLQRFARWSSNENGRPPPLTPKQKRWARTIRSEV 230







Result No.	Query No.	Score	Query			DB	ID	Description
			Match	Length	DB			
1	1143	97.5	237	2	Q6XTI8	Q6xti8 influenza a		
2	1142	97.4	237	1	VNS1_TAUSS	P03498 influenza a		
3	1142	97.4	237	2	Q6XTI4	Q6xti4 influenza a		
4	1142	97.4	237	2	Q6XTI6	Q6xti6 influenza a		
5	1142	97.4	237	2	Q6XTJ6	Q6xtj6 influenza a		
6	1141	97.4	230	1	VNS1_TALE1	P26131 influenza a		
7	1141	97.4	237	2	Q6XTJ2	P6xtj2 influenza a		
8	1140	97.3	237	1	VNS1_TAFOW	P03497 influenza a		
9	1139	97.2	237	2	Q6XTJ4	Q6xtj4 influenza a		
10	1138	97.1	237	2	Q6XTJ8	Q6xtj8 influenza a		
11	1129	96.3	230	2	Q6XTI2	Q6xti2 influenza a		
12	1128	96.2	237	1	VNS1_TACHI	P11618 influenza a		
13	1125	96.0	237	2	Q6XTJ0	Q6xtj0 influenza a		
14	1124	95.9	230	2	Q82505	Q82505 influenza a		
15	1123	95.8	233	2	Q84068	Q84068 influenza a		
16	1118	95.4	230	2	Q82506	Q82506 influenza a		
17	1116	95.2	230	2	Q67249	Q67249 influenza a		
18	1116	95.2	237	2	Q6XTH0	Q6xth0 influenza a		
19	1116	95.2	237	2	Q6XTH2	Q6xth2 influenza a		
20	1116	95.2	237	2	Q6XTH6	Q6xth6 influenza a		
21	1116	95.2	237	2	Q6XTH8	Q6xth8 influenza a		
22	1116	95.2	237	2	Q6XTI0	Q6xti0 influenza a		
23	1113	95.0	237	2	Q6XTH4	Q6xth4 influenza a		
24	1111	94.8	230	1	VNS1_TAPUE	P03496 influenza a		
25	1111	94.8	230	2	Q71QT3	Q71qt3 influenza a		
26	1110	94.7	237	2	Q6XTG8	Q6xtg8 influenza a		
27	1110	94.7	237	2	Q9DUT8	Q9dut8 influenza a		
28	1107	94.5	230	1	VNS1_TALEN	P17042 influenza a		
29	1107	94.5	230	2	Q67267	Q67267 influenza a		
30	1107	94.5	230	2	Q6LD08	Q6ld08 influenza v		
31	1107	94.5	230	2	Q76MT8	Q76mt8 influenza a		

GN Name=NS; Synonyms=8;  
 OS Influenza A virus (strain A/USSR/90/77 H1N1).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OX NCBI\_TaxID=225083;  
 RN [1]  
 RX SEQUENCE FROM N.A.  
 RP MEDLINE=83164298; PubMed=6834468;  
 RA Krystal M., Buonagurio D.A., Young J.F., Palese P.;  
 RT "Sequential mutations in the NS genes of influenza virus field  
 strains";  
 RJ J. Virol. 45:547-554 (1983).  
 RL -; ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=NS1;  
 CC IsoId=P03498-1; Sequence=Displayed;  
 CC Name=NS2;  
 CC IsoId=P03504-1; Sequence=External;  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; K00578; AAA43540.1; -;  
 DR HSSP; P03495; NS1.  
 DR InterPro; IPR000256; Flu NS1.  
 DR InterPro; IPR009068; S15/NS1\_bind.  
 DR Pfam; PF00600; Flu NS1; 1.  
 DR ProDom; PD000613; Flu NS1; 1.  
 KW Alternative splicing; Nonstructural protein.  
 SQ SEQUENCE 237 AA; 26890 MW; D5759EBE558E268 CRC64;

Query Match 97.4%; Score 1142; DB 1; Length 237;  
 Best Local Similarity 97.0%; Pred. No. 1.4e-88;  
 Matches 223; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRA 60  
 DB 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATCV 60  
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVGAPLCIRMD 120  
 DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVGAPLCIRMD 120  
 QY 121 QAIMDKSIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180  
 DB 121 QAIMDKNIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDVKNAGV 180  
 QY 181 LIGGLEWNNNTVRVSKTLQRFAMWSSNENGRPPLTPKQKRWARTIRSEV 230  
 DB 181 LIGGLEWNNNTVRVSKTLQRFAMWSSNENGRPPLTPKQKRWARTIRSEV 230

RESULT 3  
 Q6XTI4 PRELIMINARY; PRT; 237 AA.  
 AC Q6XTI4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Non-structural protein NS1.  
 OS Influenza A virus (A/Sao Paulo/3/59 (H2N2)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A; H2N2 subtype.  
 OX NCBI\_TaxID=220955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lindstrom S.E., Cox N.J., Klimov A.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY210159; AA046583.1; -;  
 DR HSSP; P03495; IAIL.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu NS1.  
 DR InterPro; IPR009068; S15/NS1\_bind.  
 DR Pfam; PF00600; Flu NS1; 1.  
 DR ProDom; PD000613; Flu NS1; 1.  
 SQ SEQUENCE 237 AA; 26972 MW; FE0004CAA50CEED7 CRC64;  
 Query Match 97.4%; Score 1142; DB 2; Length 237;  
 Best Local Similarity 96.5%; Pred. No. 1.4e-88;  
 Matches 222; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRA 60  
 DB 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRV 60  
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVGAPLCIRMD 120  
 DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVGAPLCIRMD 120  
 QY 121 QAIMDKSIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180  
 DB 121 QAIMDKNIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDVKNAGV 180  
 QY 181 LIGGLEWNNNTVRVSKTLQRFAMWSSNENGRPPLTPKQKRWARTIRSEV 230  
 DB 181 LIGGLEWNNNTVRVSKTLQRFAMWSSNENGRPPLTPKQKRWARTIRSKV 230

RESULT 4  
 Q6XTI6 PRELIMINARY; PRT; 237 AA.  
 AC Q6XTI6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Non-structural protein NS1.  
 OS Influenza A virus (A/Victoria/15681/59 (H2N2)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A; H2N2 subtype.  
 OX NCBI\_TaxID=220956;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lindstrom S.E., Cox N.J., Klimov A.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY210158; AA046581.1; -;  
 DR HSSP; P03495; IAIL.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu NS1.  
 DR InterPro; IPR009068; S15/NS1\_bind.  
 DR Pfam; PF00600; Flu NS1; 1.  
 DR ProDom; PD000613; Flu NS1; 1.  
 SQ SEQUENCE 237 AA; 26972 MW; FE0004CAA50CEED7 CRC64;  
 Query Match 97.4%; Score 1142; DB 2; Length 237;  
 Best Local Similarity 96.5%; Pred. No. 1.4e-88;  
 Matches 222; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRA 60  
 DB 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRV 60  
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVGAPLCIRMD 120  
 DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVGAPLCIRMD 120  
 QY 121 QAIMDKSIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180  
 DB 121 QAIMDKNIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDVKNAGV 180  
 QY 181 LIGGLEWNNNTVRVSKTLQRFAMWSSNENGRPPLTPKQKRWARTIRSEV 230  
 DB 181 LIGGLEWNNNTVRVSKTLQRFAMWSSNENGRPPLTPKQKRWARTIRSEV 230

Db 181 LIGLEWMDNTVRVSKTLQRFAPWRSSNENGRPPLTPKQKQWARTIRSKV 230

## RESULT 5

Q6XTJ6 PRELIMINARY; PRT; 237 AA.  
 AC Q6XTJ6  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Non-structural protein NS1.  
 OS Influenza A virus (A/Davis/1/57(H2N2)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 CC Influenzavirus A; H2N2 subtype.  
 OX NCBI\_TaxID=220951;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lindstrom S.E., Cox N.J., Klimov A.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY210153; AAO46571.1; -.  
 DR HSSP; P03495; IAIL.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu NS1.  
 DR Pfam; PF00600; S15/NS1\_bind.  
 DR ProDom; PD000613; Flu NS1; 1.  
 DR ProDom; PD000613; Flu NS1; 1.  
 SQ SEQUENCE 237 AA; 26972 MW; 88D2935CF4409ED6 CRC64;

Query Match 97.4%; Score 1142; DB 2; Length 237;  
 Best Local Similarity 96.5%; Pred. No. 1.4e-88;  
 Matches 222; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFQVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRA 60  
 Db 1 MDPNTVSSFQVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRV 60  
 Qy 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDFWMLMPKQKVGPLCIRMD 120  
 Db 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDFWMLMPKQKVGPLCIRMD 120  
 Qy 121 QAIMDKSIILKANFSVIFDLRLTLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
 Db 121 QAIMDKNIILKANFSVIFDLRLTLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
 Qy 181 LIGLEWMDNTVRVSKTLQRFAPWRSSNENGRPPLTPKQKQWARTIRSEV 230  
 Db 181 LIGLEWMDNTVRVSKTLQRFAPWRSSNENGRPPLTPKQKQWARTIRSKV 230

## RESULT 6

VNS1 IALE1 STANDARD; PRT; 230 AA.  
 AC Q6XTJ2  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Non-structural protein NS1.  
 GN Name=8;  
 OS Influenza A virus (strain A/Leningrad/134/57 H2N2).  
 OS Influenza A virus (strain A/Leningrad/134/17/57 H2N2), and  
 OS Influenza A virus (strain A/Leningrad/134/47/57 H2N2).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 CC Influenzavirus A.  
 OX NCBI\_TaxID=128148, 152281, 152282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92124758; PubMed=1733114;  
 RA Klimov A.I., Cox N.J., Yotov W.V., Rocha E., Alexandrova G.I.,  
 RA Kendal A.P.;  
 RT "Sequence changes in the live attenuated, cold-adapted variants of  
 influenza A/Leningrad/134/57 (H2N2) virus.";  
 RL Virology 186:795-797(1992).  
 CC -1- ALTERNATIVE PRODUCTS;

CC Events=Alternative splicing; Named isoforms=2;  
 CC Name=NS1;  
 CC IsoId=P26131-1; Sequence=Displayed;  
 CC Name=NS2;  
 CC IsoId=P21432-1, P26133-1;  
 CC Sequence=External;  
 CC -----  
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 CC -----  
 CC EMBL; M81572; AAA19199.1; ALT TERM.  
 DR EMBL; M81578; AAA19201.1; ALT TERM.  
 DR EMBL; M81584; AAA19203.1; ALT\_TERM.  
 DR HSSP; P03495; IANS1.  
 DR InterPro; IPR000256; Flu NS1.  
 DR InterPro; IPR009068; S15/NS1\_bind.  
 DR Pfam; PF00600; Flu NS1; 1.  
 DR ProDom; PD000613; Flu NS1; 1.  
 KW Alternative splicing; Nonstructural protein.  
 SQ SEQUENCE 230 AA; 26096 MW; D3B867B15A70CE97 CRC64;

Query Match 97.4%; Score 1141; DB 1; Length 230;  
 Best Local Similarity 96.5%; Pred. No. 1.7e-88;  
 Matches 222; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFQVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRA 60  
 Db 1 MDPNTVSSFQVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRV 60  
 Qy 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDFWMLMPKQKVGPLCIRMD 120  
 Db 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDFWMLMPKQKVGPLCIRMD 120  
 Qy 121 QAIMDKSIILKANFSVIFDLRLTLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
 Db 121 QAIMDKNIILKANFSVIFDLRLTLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180  
 Qy 181 LIGLEWMDNTVRVSKTLQRFAPWRSSNENGRPPLTPKQKQWARTIRSEV 230  
 Db 181 LIGLEWMDNTVRVSKTLQRFAPWRSSNENGRPPLTPKQKQWARTIRSKV 230

## RESULT 7

Q6XTJ2 PRELIMINARY; PRT; 237 AA.  
 AC Q6XTJ2  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Non-structural protein NS1.  
 OS Influenza A virus (A/El Salvador/2/57(H2N2)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 CC Influenzavirus A; H2N2 subtype.  
 OX NCBI\_TaxID=220952;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lindstrom S.E., Cox N.J., Klimov A.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY210155; AAO46575.1; -.  
 DR HSSP; P03495; IAIL.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu NS1.  
 DR InterPro; IPR009068; S15/NS1\_bind.  
 DR Pfam; PF00600; Flu NS1; 1.  
 DR ProDom; PD000613; Flu NS1; 1.  
 DR ProDom; PD000613; Flu NS1; 1.  
 SQ SEQUENCE 237 AA; 26943 MW; 88D293408EB944C3 CRC64;

Query Match 97.4%; Score 1141; DB 2; Length 237;

```
Best Local Similarity 96.5%; Pred. No. 1.7e-88;
Matches 222; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSGTLGLNIETAIRA 60
Db 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSGTLGLNIETATRV 60
Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120
Db 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120
Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
Qy 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSKV 230

RESULT 8
VNS1_IAPFOW STANDARD; PRT; 237 AA.
ID AC P03497;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural protein NS1.
GN Name=8;
OS Influenza A virus (strain A/Fort Warren/1/50 H1N1), and
OS Influenza A virus (strain A/RI/5-/57 H2N2).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OC NCBI_TaxID=225082, 135329;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=A/Fort Warren/1/50;
RC MEDLINE=83164298; PubMed=6834468;
RA Krystal M., Buonagurio D.A., Young J.F., Palese P.;
RT "Sequential mutations in the NS genes of influenza virus field
RT strains.";
RL J. Virol. 45:547-554(1983).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=A/RI/5-/57;
RX MEDLINE=81218398; PubMed=7241645;
RA Hall R.M., Air G.M.;
RT "Variation in nucleotide sequences coding for the N-terminal regions
RT of the matrix and nonstructural proteins of influenza A viruses.";
RL J. Virol. 38:1-7(1981).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NS1;
CC IsoId=P03497-1; Sequence=Displayed;
CC Name=NS2;
CC IsoId=P03505-1; Sequence=External;
CC -!- MISCELLANEOUS: Partial sequence of A/RI/5-/57 is identical with
CC that shown.
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CC -----
CC EMBL; K00576; AAA43525.1; -.
CC HSSP; P03495; lNS1.
CC InterPro; IPR000256; Flu_NSI.
CC InterPro; IPR009068; S15/NS1_bind.
CC Pfam; PF00600; Flu_NSI; 1.
CC ProDom; PD000613; Flu_NSI; 1.
```

```
KW Alternative splicing; Nonstructural protein.
SQ SEQUENCE 237 AA; 26889 MW; 3B80159BFD79F212 CRC64;

Query Match 97.3%; Score 1140; DB 1; Length 237;
Best Local Similarity 96.5%; Pred. No. 2.1e-88;
Matches 222; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSGTLGLNIETAIRA 60
Db 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSGTLGLNIETATRV 60
Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120
Db 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120
Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
Qy 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230

RESULT 9
Q6XTJ4 PRELIMINARY; PRT; 237 AA.
ID AC Q6XTJ4;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Non-structural protein NS1.
OS Influenza A virus (A/Chile/13/57(H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OC NCBI_TaxID=221934;
OX [1]
RN SEQUENCE FROM N.A.
RP Lindstrom S.E., Cox N.J., Klimov A.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY210154; AAC46573.1; -.
DR HSSP; P03495; lAIL.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu_NSI.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu_NSI; 1.
DR ProDom; PD000613; Flu_NSI; 1.
DR SEQUENCE 237 AA; 27004 MW; 29158F21429BF365 CRC64;

Query Match 97.2%; Score 1139; DB 2; Length 237;
Best Local Similarity 96.1%; Pred. No. 2.5e-88;
Matches 221; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSGTLGLNIETAIRA 60
Db 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPFLDLRLRDQKSLRGSGTLGLNIETATRV 60
Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120
Db 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120
Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
Qy 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSKV 230

RESULT 10
Q6XTJ8 PRELIMINARY; PRT; 237 AA.
ID AC Q6XTJ8
```

Db	1	MDSNTVSSFOVDCFLVHVRKQVADQELGDAPFLDLRLRRDQKSLGRGSTLGLNIETATRV	60
Qy	61	GKQIVERILKEESDEALKWMTMASAPASRYLTDMTIEMSRDWFMLMPKQKVAGPLCIRMD	120
Db	61	GKQIVERILKEESNEALKWMTMASTPASRYLTDMTIEMSRDWFMLMPKQKVAGPLCIRMD	120
Qy	121	QAIMDKSIILKANFSVIFORLETLILLRAPTEGAIVGEISPLSPFGHTNEDIKNAIGV	180
Db	121	QAIMDKNIILKANFSVIFORLETLILLRAPTEGAIVGEISPLSPFGHTNEDVQNAIGV	180
Qy	181	LIGGLENNNTVRVSTIQFPAWRSSNENGRPPLTPKQKRMARTIRSEV	230
Db	181	LIGGLENDNTVRVSTLQFPAWRSSNENGRPPLTPKQKRMARTIRSKV	230

RESULT 12

VNSI\_IACHI

ID	VNSI_IACHI	STANDARD;	PRT;	237	AA.
AC	P11618;				
DT	01-OCT-1989	(Rel. 12, Created)			
DT	01-NOV-1990	(Rel. 16, Last sequence update)			
DT	25-OCT-2004	(Rel. 45, Last annotation update)			
DE	Nonstructural protein NS1.				
GN	Name=8;				
OS	Influenza A virus (strain A/Chile/1/83 H1N1).				
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;				
OC	Influenzavirus A.				
OX	NCBI_TaxID=241242;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89345097; PubMed=2762132;				
RA	Schreier E., Roeske H., Michel S.;				
RT	"Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83				
RT	(H1N1)".				
RL	Nucleic Acids Res. 17:5381-5381(1989).				
CC	-1- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=2;				
CC	Name=NS1;				
CC	IsoId=P11618-1; Sequence=Displayed;				
CC	Name=NS2;				
CC	IsoId=P11619-1; Sequence=External;				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL; X15282; CAA33355.2; --				
DR	HSSP; P03495; NS1.				
DR	InterPro; IPR000256; Flu NS1.				
DR	InterPro; IPR009068; S15/NS1_bind.				
DR	Pfam; PF00600; Flu NS1; 1.				
DR	ProDom; PD000613; Flu NS1; 1.				
DR	Alternative splicing; Nonstructural protein.				
SK	Sequence 237 AA; 26819 MW; C33A9E3D0386E752 CRC64;				

Query Match

Best Local Similarity

Matches 219; Conservative

96.2%; Score 1128; DB 1; Length 237;

95.2%; Pred. No. 2.2e-87;

7; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MDPNTVSSFOVDCFLVHVRKRVADQELGDAPFLDLRLRRDQKSLGRGSTLGLNIETAIRA	60
Db	1	MDPNTVSSFOVDCFLVHVRKQVADQELGDAPFLDLRLRRDQKSLGRGSTLGLDIETATCV	60
Qy	61	GKQIVERILKEESDEALKWMTMASAPASRYLTDMTIEMSRDWFMLMPKQKVAGPLCIRMD	120
Db	61	GKQIVERILKEESDEALKWMTMASAPASRYLTDMTIEMSRDWFMLMPKQKVAGPLCVRMD	120
Qy	121	QAIMDKSIILKANFSVIFORLETLILLRAPTEGAIVGEISPLSPFGHTNEDIKNAIGV	180

```

Db 121 QAIMDKNIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTNEDVKNAGV 180
QY 181 LIGGLEWNNNTVRVSKTLQRFARSSNENGRPLTPKQKRWARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFARSSNENGRPLTPKQKRWARTIRSEV 230

RESULT 13
Q6XTJ0 PRELIMINARY; PRT; 237 AA.
AC Q6XTJ0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Non-structural protein NS1.
OS Influenza A virus (A/Malaya/16/58 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220954;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210156; AA046577.1; -.
DR HSSP; P03495; 1A1L.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu_NSI.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu_NSI; 1.
DR ProDom; PD000613; Flu_NSI; 1.
SQ SEQUENCE 237 AA; 26940 MW; 60B8C406AFD784C9 CRC64;

Query Match 96.0%; Score 1125; DB 2; Length 237;
Best Local Similarity 95.2%; Pred. No. 3.9e-87; Mismatches 5; Indels 0; Gaps 0;
Matches 219; Conservative 6;

QY 1 MDPNTVSSFQVDCFLMHWKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETATRA 60
Db 1 MDPNTVSSFQVDCFLMHWKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETATRV 60
QY 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEMSRDWFMMPKQKVGAPLCIRMD 120
Db 61 GKQIVERILKEESDEALKMTMASAPASRYLNDMTIEMSRDWFMMPKQKVGAPLCIRMD 120
QY 121 QAIMDKSIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTNEDVKNAGV 180
QY 181 LIGGLEWNNNTVRVSKTLQRFARSSNENGRPLTPKQKRWARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFARSSNENGRPLTPKQKRWARTIRSKV 230

RESULT 14
Q82505 PRELIMINARY; PRT; 230 AA.
AC Q82505;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Non-structural protein 1.
CN Name=NS1;
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=WSN/40; TISSUE=Mouse;
RA Husak P.J., Schlesinger R.W.;
RT "Replication of neurovirulent and non-neurovirulent human HN1
influenza A viruses in mouse brain and nerve cell cultures: virus

```

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strain-specific and host cell-dependent variations in progeny virus
asse.";
RL Thesis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert
Wood Johnson Medical School.
DR EMBL; U13682; AAA21580.1; -.
DR HSSP; P03495; 1NS1.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu_NSI.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu_NSI; 1.
DR ProDom; PD000613; Flu_NSI; 1.
SQ SEQUENCE 230 AA; 26040 MW; 03D355F2EA3AC5A8 CRC64;

Query Match 95.9%; Score 1124; DB 2; Length 230;
Best Local Similarity 94.8%; Pred. No. 4.6e-87;
Matches 218; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDPNTVSSFQVDCFLMHWKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETATRA 60
Db 1 MDPNTVSSFQVDCFLMHWKRVADQELGDPFLDRLRDQKSLRGSGTLGLDIETATRA 60
QY 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEMSRDWFMMPKQKVGAPLCIRMD 120
Db 61 GKQIVERILKEESDEALKMTMASVPASRYLTDMTLEMSRHWFMMPKQKVGAPLCIRMD 120
QY 121 QAIMDKSIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTDVEDVKNAGV 180
QY 181 LIGGLEWNNNTVRVSKTLQRFARSSNENGRPLTPKQKRWARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSETLQRFARSSNENGRPLTPKQKRWAGTIRSEV 230

RESULT 15
Q84068 PRELIMINARY; PRT; 233 AA.
AC Q84068;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Nonstructural protein 1 (Fragment).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86208139; PubMed=2939560;
RA Buonagurio D.A., Nakada S., Parvin J.D., Krystal M., Palese P.,
RA Fitch W.M.;
RT "Evolution of human influenza A viruses over 50 years: rapid, uniform
rate of change in NS gene.";
RL Science 232:380-382(1986).
DR EMBL; M12592; AAA43506.1; -.
DR HSSP; P03495; 1NS1.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR000256; Flu_NSI.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu_NSI; 1.
DR ProDom; PD000613; Flu_NSI; 1.
KW Nonstructural protein.
RN NON TER 1
SQ SEQUENCE 233 AA; 26485 MW; 1C345B24E04D617D CRC64;

Query Match 95.8%; Score 1123; DB 2; Length 233;
Best Local Similarity 96.9%; Pred. No. 5.6e-87;
Matches 219; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVSSFQVDCFLMHWKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETATRAKQI 64
Db 1 TVSSFQVDCFLMHWKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETATRVGKQI 60

```

Qy	65	VERILKEESDEALKQWTMASAPASRYLTDMTTEMSRDWFMMPKQKVAGPLCIRMDQAIM	124
Db	61	VERILKEESDEALKQWTMASAPASRYLTDMTTEMSRDWFMMPKQKVAGPLCIRMDQAIM	120
Qy	125	DKSIILKANFSVIPDRLETLILLRAFTTEGAIUGEISPLSLPGHTNEDIKNAIGVLIGG	184
Db	121	DKNIILKANFSVIPDRLETLILLRAFTTEGAIUGEISPLSLPGHTNEDVNAIGVLIGG	180
Qy	185	LEWNNNTVRSKTLQRFARSSNENGRPPLTPKQKQKVARTIRSEV	230
Db	181	LEWNDNTVRSKTLQRFARSSNENGRPPLTPKQKQKVARTIRSEV	226

Search completed: September 22, 2005, 21:46:05  
Job time : 145.504 secs

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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:28:42 ; Search time 82.3903 Seconds  
(without alignments)  
568.004 Million cell updates/sec

Title: US-10-654-737-6

Perfect score: 607

Sequence: 1 MDPNTVSSFDILMRISKWQ.....ALQLLVEQIRTFESFQLI 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: geneseq1980s.\*

2: geneseq1990s.\*

3: geneseq2000s.\*

4: geneseq2001s.\*

5: geneseq2002s.\*

6: geneseq2003as.\*

7: geneseq2003bs.\*

8: geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	97.2	121	5	Aae23117 Influenza
2	575	94.7	121	5	Abb05773 Influenza
3	96.5	15.9	880	4	Ab96332 Putative
4	96.5	15.9	880	8	Ad543213 Bacterial
5	86	14.2	819	4	Aam40442 Human pol
6	86	14.2	819	4	Aam40443 Human pol
7	86	14.2	819	8	Ad511970 Human the
8	86	14.2	819	8	Ad511971 Human the
9	86	14.2	819	8	Ad511969 Human the
10	86	14.2	819	8	Ad511968 Human the
11	84	13.8	122	5	Aae23128 Influenza
12	83.5	13.8	1179	8	Ad541964 Bacterial
13	83.5	13.8	1179	8	Adn18677 Bacterial
14	83	13.7	996	4	Abb71614 Drosophil
15	82.5	13.6	236	7	Adn95580 Human BEC
16	82	13.5	350	2	Aay37571 Chlamydia
17	82	13.5	561	2	Aaw63043 Streptoco
18	82	13.5	876	7	Adm26084 Hyperther
19	81	13.3	156	2	Aar03991 Mr 25K in
20	81	13.3	498	7	Adf74149 Human nov
21	81	13.3	653	8	Adq66256 Novel hum
22	81	13.3	872	5	Aao22902 Phosphati
23	81	13.3	872	5	Abu65076 Human NOV
24	81	13.3	872	8	Adn61803 Human nov
25	81	13.3	874	5	Abp69419 Human pol

26	81	13.3	874	5	ABG31896	Abg31896 Human lip
27	81	13.3	874	5	AAU79749	Aau79749 Human pho
28	81	13.3	881	8	ADQ66093	Adq66093 Novel hum
29	81	13.3	902	5	ABG31895	Abg31895 Human lip
30	81	13.3	902	5	AAU79750	Aau79750 Human pho
31	80.5	13.3	163	4	ABG06887	Abg06887 Novel hum
32	80.5	13.3	944	6	ABR53314	ABr53314 Protein s
33	80.5	13.3	944	7	ADK63498	Adk63498 Disease t
34	80.5	13.3	944	8	ADN19029	Adn19029 Bacterial
35	80	13.2	376	8	ADN22707	Adn22707 Bacterial
36	80	13.2	875	5	AAO22903	Aao22903 Phosphati
37	80	13.2	952	7	ADJ69356	Adj69356 Human hea
38	80	13.2	962	3	AB13326	Ab13326 Caenorhab
39	80	13.2	1131	8	ABM80698	ABm80698 Tumour-as
40	80	13.2	1253	4	AA47149	AA47149 CDIFF-8,
41	80	13.2	1281	8	ADP55147	Adp55147 Human PRO
42	80	13.2	1281	8	ADP24771	Adp24771 PRO polyp
43	77.5	12.8	331	7	ADF06826	Adf06826 Bacterial
44	77.5	12.8	777	8	ADQ66447	Adq66447 Novel hum
45	77.5	12.8	2000	8	ADN03898	Adn03898 Antipsori

#### ALIGNMENTS

RESULT 1  
AAE23117  
ID AAE23117 standard; protein; 121 AA.  
XX AC AAE23117;  
XX AC  
DT 21-AUG-2002 (first entry)  
DE Influenza A virus/singapore/1/57/ca NS2 mutant protein.  
XX DE  
KW Attenuated influenza vaccine; prophylactic; therapeutic; infection;  
KW virucide; mutant; mutein; NS2 protein.  
XX OS  
OS Influenza A virus.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Misc-difference 8..9 /note= "Encoded by 48-525 bases"  
XX FT  
XX WO200224876-A2.  
XX PD 28-MAR-2002.  
XX XX  
XX 25-SEP-2001; 2001WO-EP011087.  
XX XX  
XX 25-SEP-2000; 2000EP-00120896.  
XX XX  
XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.  
XX XX  
XX Katinger H, Egorov A, Ferko B, Romanova J, Katinger D;  
XX WPI; 2002-416282/44.  
XX N-PSDB; AAD37061.  
XX XX  
XX Manufacturing live vaccine, by infecting Vero cells with virus, combining  
XX cells with serum-free cell culture medium, incubating cells in presence  
XX of protease and nuclease, harvesting virus and preparing vaccine.  
XX Example 4; Page 63; 90pp; English.  
XX XX  
XX The present invention relates to a method for isolating viruses from  
XX various sources and for producing live attenuated influenza vaccines in a  
XX serum-free African Green monkey kidney (Vero) cell culture under  
XX conditions where alterations in the surface antigens of the virus due to  
XX adaptive selection are minimised or prevented. The method is useful for  
XX the manufacture of whole-virus vaccine, preferably attenuated live  
XX vaccine. It is useful for prophylactic or therapeutic administration







CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification  
 XX Sequence 819 AA;  
 SQ

Query Match 14.2%; Score 86; DB 4; Length 819;  
 Best Local Similarity 21.5%; Pred. No. 2.1;  
 Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps 4;

Qy 19 MQLGSSSEDLNGIITQFESLKLRYDSLGEAVM-RMGDLHSLQNRNGKWEQLGQ----- 71  
 Db 537 LPIGTASADVAAADIAK-----YTSKLMDAIKGTMTIYNDLSKNTTWKQALEDQSGLR 590

Qy 72 -KFEIRWL-----IEEVRLKIKITENSFEQITFMQALQLLLEVEOEI 113  
 Db 591 IEIEKQLWLHQOELSEMKNLELTWAEMRQSWEQERDLIAEVKKQL 637

RESULT 6  
 AAM40443  
 ID AAM40443 standard; protein; 819 AA.  
 XX  
 AC AAM40443;  
 DT  
 DT 22-OCT-2001 (first entry)  
 DE Human polypeptide SEQ ID NO 5374.  
 XX  
 KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US034263.  
 XX  
 PR 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-0048725.  
 PR 25-APR-2000; 2000US-0052317.  
 PR 20-JUN-2000; 2000US-00598042.  
 PR 19-JUL-2000; 2000US-00620312.  
 PR 03-AUG-2000; 2000US-00653450.  
 PR 14-SEP-2000; 2000US-00662191.  
 PR 19-OCT-2000; 2000US-00693036.  
 PR 29-NOV-2000; 2000US-00727344.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 PI Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 DR N-PSDB; AAI59599.  
 XX  
 XX Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.  
 XX  
 PS Example 2; SEQ ID NO 5374; 10078pp; English.

XX The invention relates to human nucleic acids (AAI5798-AAI61369) and the  
 CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification  
 XX Sequence 819 AA;  
 SQ

Query Match 14.2%; Score 86; DB 4; Length 819;  
 Best Local Similarity 21.5%; Pred. No. 2.1;  
 Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps 4;

Qy 19 MQLGSSSEDLNGIITQFESLKLRYDSLGEAVM-RMGDLHSLQNRNGKWEQLGQ----- 71  
 Db 537 LPIGTASADVAAADIAK-----YTSKLMDAIKGTMTIYNDLSKNTTWKQALEDQSGLR 590

Qy 72 -KFEIRWL-----IEEVRLKIKITENSFEQITFMQALQLLLEVEOEI 113  
 Db 591 IEIEKQLWLHQOELSEMKNLELTWAEMRQSWEQERDLIAEVKKQL 637

RESULT 7  
 ADS11970  
 ID ADS11970 standard; protein; 819 AA.  
 XX  
 AC ADS11970;  
 DT  
 DT 16-DEC-2004 (first entry)  
 XX  
 DB Human therapeutic contig protein - SEQ ID 2207.  
 XX  
 KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
 KW aplastic anaemia; cancer; wound healing; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..819  
 FT /label= Unknown, OTHER  
 FT /note= "OTHER = In-frame STOP codon"  
 XX  
 PN WO2004080148-A2.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 30-SEP-2003; 2003WO-US030720.  
 XX  
 PR 02-OCT-2002; 2002US-0416186P.  
 XX  
 PA (NUVE-) NUVELO INC.  
 XX  
 PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;  
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
 XX  
 DR WPI; 2004-668857/65.  
 DR N-PSDB; ADS11372.  
 XX  
 XX New polynucleotide, useful in preparing a composition for diagnosing or  
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
 PT aplastic anemia or cancer for promoting wound healing.  
 XX

PS Example 2; SEQ ID NO 2207; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded  
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may  
CC be useful in preparing a composition for diagnosing or treating  
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
CC disorders, such as aplastic anaemia or cancer, as well as for promoting  
CC wound healing. The molecules may also be utilised during gene therapy  
CC procedures. The current sequence is that of a human therapeutic contig  
CC protein of the invention.

XX Sequence 819 AA;

Query Match 14.2%; Score 86; DB 8; Length 819;

Best Local Similarity 21.5%; Pred. No. 2.1;

Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps 4;

QY 19 MQLGSSSEDLNGIITQESLKLKRDLSGEAVM-RMGDLHSLQNGKWRQELGQ----- 71

DB 537 LPIGTASADVAADIAK-----YTSKLMDAIKGMTIYNDLSKNTTWKQAQLAESDQGLR 590

QY 72 -KPEEIRWL-----IEVVRHLKITEFSFEQITFMQALQLLLEVRQEI 113

DB 591 IEIEKQLWLHQQLSEKKNLELTMAEMRQSWEQERDLIAEVKKQL 637

RESULT 8

ADSL1971

ID ADSL1971 standard; protein; 819 AA.

XX AC ADSL1971;

XX DT 16-DEC-2004 (first entry)

XX DE Human therapeutic contig protein - SEQ ID 2208.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
XX aplastic anaemia; cancer; wound healing; gene therapy.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 1. .819

XX /label= Unknown, OTHER

XX /note= "OTHER = In-frame STOP codon"

XX W02004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;

XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX WPI; 2004-668857/65.

XX N-PSDB; ADS11373.

XX New polynucleotide, useful in preparing a composition for diagnosing or  
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
XX aplastic anaemia or cancer for promoting wound healing.

XX Example 2; SEQ ID NO 2208; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded  
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may

CC

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CC

CC

CC

CC



Matches 34; Conservative 24; Mismatches 44; Indels 34; Gaps 6;  
QY 4 NTVSFDDILMRISKMGSSSED-----LNGIITQPSLKLYRDSLGAVRMGDLHSLQ 59  
DB 3 NNITTTQ-IEWRMKKAIGSTHSSSSVLMKDIQSFQQLRWESYPLNV-KSTDYH--- 57  
QY 60 NRMGKWEQLGQKFEIRWLEEVH-----HRLKITENSF--EQITFMQALQL 105  
DB 58 -----QKRETKLVTEELYLLSKRIDNLFHKTIVIANSSIIADNVVSLLET 106  
QY 106 LLEVEQBIRTFSQLI 121  
DB 107 LYEMKDVVEYSROCL 122  
RESULT 12  
ADS41964  
ID ADS41964 standard; protein; 1179 AA.  
AC ADS41964;  
XX  
XX 02-DEC-2004 (first entry)  
DB Bacterial polypeptide #20394.  
XX Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX Bacteria.  
OS US2003233675-A1.  
XX 18-DEC-2003.  
XX 20-FEB-2003; 2003US-00369493.  
XX 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX Claim 1; SEQ ID NO 20394; 122pp; English.  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
XX Sequence 1179 AA;

Query Match 13.8%; Score 83.5; DB 8; Length 1179;  
Best Local Similarity 23.9%; Pred. No. 6.6; Mismatches 44; Indels 15; Gaps 3;  
Matches 27; Conservative 27;  
QY 23 SSSDNLNGIITQF-----ESLKLYRDSLGAVRMGDLHSLQNRNGKWEQLGQ 71  
DB 825 SLEEEIEGLVKNKALKANINENEALKSJTEKLEKKEGEIYSRIEEQKKKEELER 884  
QY 72 KFEIRWLEEVHHR---LKITENSFEQITFMQALQLLLEVEQBIRTFSQLI 121  
DB 885 KVAELREEKEKISRRIQELRAIEVNTL-KVRNSQLKSLMEKNSQLKHSKEVI 936

RESULT 13  
ADN18677  
ID ADN18677 standard; protein; 1179 AA.  
XX  
AC ADN18677;  
XX 02-DEC-2004 (first entry)  
DB Bacterial polypeptide #1330.  
XX Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX Bacteria.  
OS US2003233675-A1.  
XX 18-DEC-2003.  
XX 20-FEB-2003; 2003US-00369493.  
XX 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
PI WPI; 2004-061375/06.  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX Claim 1; SEQ ID NO 1330; 122pp; English.  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 1179 AA;

Query Match 13.8%; Score 83.5; DB 8; Length 1179;  
Best Local Similarity 23.9%; Pred. No. 6.6;  
Matches 27; Conservative 27; Mismatches 44; Indels 15; Gaps 3;

QY 23 SSEDNLNGIITQF-----ESLKYRDSIGEAVMGDLHSLONRNGKWRQLQ 71  
DB 825 SLEEIEGLVKNKALKANINENEAUKSTLEKLUKKEGEIYRIEIQKKKCELER 884  
QY 72 KPEIRKWLIEVRHR---LKITENSFEQITFMQALQLLLEVEQIRTFSPQLI 121  
DB 885 KVAREEKEKISRRIQELIEVNTL-KVNSQLKSLMEKNSQLKHFSKEVI 936

RESULT 14

ABBB71614  
ID ABB71614 standard; protein; 996 AA.

XX ABB71614;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 41634.

XX Drosophila; developmental biology; cell signalling; insecticide;  
XX pharmaceutical.

XX Drosophila melanogaster.

XX W0200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL15717.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions.

XX Disclosure; SEQ ID NO 41634; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at fcp.wipo.int/pub/published\_pct\_sequences

XX Sequence 996 AA;

Query Match 13.7%; Score 83; DB 4; Length 996;  
Best Local Similarity 26.1%; Pred. No. 6;  
Matches 31; Conservative 25; Mismatches 39; Indels 24; Gaps 5;

QY 2 DNTVSSFDILMRISKMQLGSSSEDLNGIITQFESLKYRDSIGEAVMRMDLH----- 56  
DB 824 DPEQI---QQLQSGVGLQ---SGEGLEG-----ETLQMTDGSQGMVLVHGDNNOQLI 872  
QY 57 --SLQNRNGKREQLGQKFEIRWLIEVRHLKITENSFEQITFMQALQLLLEVEQEI 113  
DB 873 DASLLNSEQLLIQQQDGEENHVISDGTIRIPVS-----VSYTEDGQPIVQVQQV 925

RESULT 15

ADN95580  
ID ADN95580 standard; protein; 236 AA.

XX ADN95580;

XX 01-JUL-2004 (first entry)

XX Human BEC/LEC-related protein sequence SeqID503.

XX growth; differentiation; blood endothelial cell; BEC;  
XX lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;  
XX lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytosstatic;  
XX vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;  
XX inflammatory disease; cancer metastasis; lymphatic system; human.

XX Homo sapiens.

XX W02003080640-A1.

XX 02-OCT-2003.

XX 07-MAR-2003; 2003WO-US006900.

XX 07-MAR-2002; 2002US-0363019P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (LICN ) LICENTIA LTD.

XX Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;

XX WPI; 2003-876899/81.

XX N-PSDB; ADN95581.

XX Example 1; SEQ ID NO 503; 176pp; English.

XX This invention relates to a method of differentially modulating the  
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic  
CC endothelial cells (LEC) comprises contacting endothelial cells with a  
CC composition comprising an agent that differentially modulates blood or  
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises  
CC identifying a human subject with lymphoedema and with a mutation in at  
CC least one allele of a gene encoding a LEC protein, where the mutation  
CC correlates with lymphoedema in human subjects, and with the proviso that  
CC the LEC protein is not VEGFR-3; and administering to the subject a  
CC composition comprising a lymphatic growth agent selected from VEGF-C or





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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:33:28 ; Search time 16.8917 Seconds  
(without alignments)  
689.226 Million cell updates/sec

Title: US-10-654-737-6

Perfect score: 607

Sequence: 1 MDPNTVSSFDILMRISKMQ.....ALQLLVEQEIRTFSQLI 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	98.4	121	1 MNIV2A	nonstructural prot
2	596	98.2	121	2 S33685	nonstructural prot
3	594	97.9	121	1 MNIV62	nonstructural prot
4	588	96.9	121	1 MNIV2M	nonstructural prot
5	587	96.7	121	1 MNIVC2	nonstructural prot
6	586	96.5	121	1 MNIV2W	nonstructural prot
7	575	94.7	121	1 B45539	nonstructural prot
8	575	94.7	121	1 MNIV2K	nonstructural prot
9	574	94.6	121	2 S09649	NS2 protein - infl
10	569	93.7	118	1 MNIVXK	nonstructural prot
11	567	93.4	121	1 MNIVX4	nonstructural prot
12	564	92.9	118	1 MNIVX2	nonstructural prot
13	564	92.9	118	1 MNIVX8	nonstructural prot
14	564	92.9	121	1 MNIVB4	nonstructural prot
15	563	92.8	121	1 MNIVB1	nonstructural prot
16	559	92.1	121	1 MNIVB3	nonstructural prot
17	556	91.6	118	1 MNIVX2	nonstructural prot
18	549	90.4	118	1 MNIVX6	nonstructural prot
19	517	85.2	108	1 MNIV2F	nonstructural prot
20	486	80.1	121	1 MNIV26	nonstructural prot
21	478	78.7	121	2 B45575	nonstructural prot
22	475	78.3	121	1 MNIVB7	nonstructural prot
23	473	77.9	121	1 MNIVB5	nonstructural prot
24	468	77.1	121	1 MNIVB6	nonstructural prot
25	467	76.9	121	1 MNIVB8	nonstructural prot
26	96.5	15.9	880	2 F75103	conserved hypothet
27	88	14.5	2541	2 T29340	hypothetical prote
28	83.5	13.8	1179	2 F71190	probable chromosom
29	82.5	13.6	122	1 MNIVB	nonstructural prot

## ALIGNMENTS

## RESULT 1

MNIV2A

nonstructural protein NS2 - influenza A virus (strain A/USSR/90/77 [H1N1])

C;Species: influenza A virus

C;Date: 31-Oct-1980 #sequence\_revision 14-Nov-1983 #text\_change 16-Jul-1999

C;Accession: B92991; A04095; A90801; C92991; D92991

R;Krystal, M.; Buonagurio, D.; Young, J.P.; Palese, P.

J. Virol. 45, 547-554, 1983

A;Title: Sequential mutations in the NS genes of influenza virus field strains.

A;Reference number: A92991; MUID:83164298; PMID:6834468

A;Accession: B92991

A;Molecule type: genomic RNA

A;Residues: 1-121 <RKY>

A;Cross-references: GB:K00578; NID:g324839; PIDN:AAA43539.1; PID:g324840

C;Genetics:

A;Map position: segment 8

C;Superfamily: Influenza virus nonstructural protein NS2

C;Keywords: alternative splicing

Query Match 98.4%; Score 597; DB 1; Length 121;  
Best Local Similarity 97.5%; Pred.No. 2.6e-44;  
Matches 118; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	1	MDPNTVSSFDILMRISKMQLGSSSEDNGITQFESLKYRDSLGAVNRMGDLHSLQN	60
DB	1	MDPNTVSSFDILMRISKMQLGSSSEDNGITQFESLKYRDSLGAVNRMGDLHSLQN	60
QY	61	RNGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLVEQEIRTFSQL	120
DB	61	RNGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLVEQEIRTFSQL	120
QY	121	I 121	
DB	121	I 121	

## RESULT 2

S33685

nonstructural protein NS1 - influenza A virus (strain A/WS/33)

C;Species: influenza A virus

A;Variety: strain A/WS/33

C;Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004

C;Accession: S33685; S32221

R;Ward, A.C.; Azad, A.A.; Macreadie, I.G.; McKimm-Breschkin, J.L.

Nucleic Acids Res. 21, 2257, 1993

A;Title: Complete nucleotide sequence of the non-structural gene of the human influenza

A;Reference number: S33685; MUID:93275765; PMID:8502573

A;Accession: S33685

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-121 <WAR>

A;Cross-references: UNIPROT:Q06049; EMBL:Z21498; NID:g296585; PIDN:CAA79707.1; PID:g2965.

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993  
 C;Genetics:  
 A;Map position: segment 8  
 C;Superfamily: influenza virus nonstructural protein NS2  
 C;Keywords: alternative splicing

Query Match 98.2%; Score 596; DB 2; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 3.1e-44;  
 Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKQMGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKQMGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

Qy 61 RKGKWEQLGQKQFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWEQLGQKQFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

#### RESULT 3

MNV62

nonstructural protein NS2 - influenza A virus (strain A/Ann Arbor/6/60 [H2N2])

C;Species: influenza A virus

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Jul-1999

C;Accession: H31831

R;Cox, N.J.; Kitame, F.; Kendal, A.P.; Maassab, H.F.; Naeve, C.

Virology 167, 554-567, 1988

A;Title: Identification of sequence changes in the cold-adapted, live attenuated influenza

A;Reference number: A31831; MUID:89073759; PMID:2974219

A;Accession: H31831

A;Molecule type: genomic RNA

A;Residues: 1-121 <CX>

A;Cross-references: GB:M23968; GB:J04349; GB:M23969; NID:G324860; PIDN:AAA43552.1; PID:9

C;Genetics:

A;Map position: segment 8

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing; nonstructural protein

Query Match 97.9%; Score 594; DB 1; Length 121;  
 Best Local Similarity 96.7%; Pred. No. 4.6e-44;  
 Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKQMGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKQMGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

Qy 61 RKGKWEQLGQKQFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWEQLGQKQFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

#### RESULT 4

MNV2M

nonstructural protein NS2 - influenza A virus (strain A/FM/1/47 [H1N1])

C;Species: influenza A virus

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 16-Jul-1999

C;Accession: D92991; A04095

R;Krystral, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A;Title: Sequential mutations in the NS genes of influenza virus field strains.

A;Reference number: A92991; MUID:83164298; PMID:6834468

A;Accession: D92991

A;Molecule type: genomic RNA

A;Residues: 1-121 <KRY>

A;Cross-references: GB:K00576; NID:G324813; PIDN:AAA43524.1; PID:G324814

C;Genetics:

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing

Query Match 96.9%; Score 588; DB 1; Length 121;  
 Best Local Similarity 95.9%; Pred. No. 1.5e-43;  
 Matches 116; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKQMGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKQMGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

Qy 61 RKGKWEQLGQKQFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWEQLGQKQFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

#### RESULT 5

MNV2C

nonstructural protein NS2 - influenza A virus (strain A/Chile/1/83 [H1N1])

C;Species: influenza A virus

C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 16-Jul-1999

C;Accession: B34215; S04837

R;Schreier, E.; Roewe, H.; Michel, S.

Nucleic Acids Res. 17, 5381, 1989

A;Title: Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83 (H1N1).

A;Reference number: A34215; MUID:89345097; PMID:2762132

A;Accession: B34215

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-121 <SCH>

A;Cross-references: EMBL:X15282; NID:G60479; PIDN:CAA33356.1; PID:G60481

C;Genetics:

A;Map position: segment 8

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing; nonstructural protein

Query Match 96.7%; Score 587; DB 1; Length 121;  
 Best Local Similarity 95.9%; Pred. No. 1.8e-43;  
 Matches 116; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKQMGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKQMGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

Qy 61 RKGKWEQLGQKQFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWEQLGQKQFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

#### RESULT 6

MNV2W

nonstructural protein NS2 - influenza A virus (strain A/FW/1/50 [H1N1])

C;Species: influenza A virus

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 24-Sep-1999

C;Accession: C92991; A04095

R;Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A;Title: Sequential mutations in the NS genes of influenza virus field strains.

A;Reference number: A92991; MUID:83164298; PMID:6834468

A;Accession: C92991

A;Molecule type: genomic RNA

A;Residues: 1-121 <KRY>

A;Cross-references: GB:K00577; NID:G324808; PIDN:AAA43521.1; PID:G324809  
C;Genetics:  
A;Map position: segment 8  
C;Superfamily: influenza virus nonstructural protein NS2  
C;Keywords: alternative splicing

Query Match 96.5%; Score 586; DB 1; Length 121;  
Best Local Similarity 95.9%; Pred. No. 2.2e-43;  
Matches 116; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKMQLGSSSEDLNGIITQFESLKYRDSLGAVMRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKMQLGSSSEDLNGIITQFESLKYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGKWRQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWRQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

#### RESULT 7

E45539

nonstructural protein NS2 - influenza A virus (strain A/chicken/Brescia/1902 [H7N7])

C;Species: influenza A virus

C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 26-May-1994

C;Accession: E45539

R;Klimov, A.; Prosch, S.; Schafer, J.; Bucher, D.

Arch. Virol. 122, 143-161, 1992

A;Title: Subtype H7 influenza viruses: comparative antigenic and molecular analysis of

A;Reference number: A45539; MUID:92109567; PMID:1530908

A;Accession: E45539

A;Molecule type: genomic RNA

A;Residues: 1-121 <KUI>

A;Note: sequence extracted from NCBI backbone (NCBIN:74250, NCBIP:74255)

C;Genetics:

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing

Query Match 94.7%; Score 575; DB 1; Length 121;  
Best Local Similarity 94.2%; Pred. No. 2e-42;  
Matches 114; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKMQLGSSSEDLNGIITQFESLKYRDSLGAVMRMGDLHSLQN 60

Db 1 MDSNTVSSFDILMRISKMQLGSSSEDLNGMITQFETLKYRDSLGAVMRIGDLHSLQS 60

Qy 61 RKGKWRQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWRQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

#### RESULT 8

MNIV2K

nonstructural protein NS2 - influenza A virus (strains A/Alaska/6/77 and A/Udorn/72 [H3N

C;Species: influenza A virus

A;Note: host Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 09-Jul-2004

C;Accession: A04094; A90801; A04095

R;Buonsquiro, D.A.; Krystal, M.; Palese, P.; DeBorde, D.C.; Maassab, H.F.

J. Virol. 49, 418-425, 1984

A;Title: Analysis of an influenza A virus mutant with a deletion in the NS segment.

A;Reference number: A92994; MUID:84115066; PMID:6363726

A;Accession: A04094

A;Molecule type: genomic RNA

A;Residues: 1-121 <BUO>

A;Cross-references: UNIPROT:P03503; GB:K01332; NID:G324795; PIDN:AAA43514.1; PID:G324796  
A;Experimental source: strain A/Alaska/6/77  
R;Lamb, R.A.; Lai, C.J.

Cell 21, 475-485, 1980

A;Title: Sequence of interrupted and uninterrupt mRNA and cloned DNA coding for the v

A;Reference number: A90801; MUID:81001890; PMID:7407920

A;Accession: A90801

A;Molecule type: genomic RNA

A;Residues: 1-121 <LAM>

A;Cross-references: GB:V01102; GB:J02169; NID:G60797; PIDN:CAA24289.1; PID:G60799

A;Experimental source: strain A/Udorn/72 [H3N2]

C;Genetics:

A;Map position: segment 8

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing

Query Match 94.7%; Score 575; DB 1; Length 121;  
Best Local Similarity 94.2%; Pred. No. 2e-42;  
Matches 114; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKMQLGSSSEDLNGIITQFESLKYRDSLGAVMRMGDLHSLQN 60

Db 1 MDSNTVSSFDILMRISKMQLGSSSEDLNGMITQFESLKYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGKWRQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWRQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

#### RESULT 9

S09649

NS2 protein - influenza A virus

C;Species: influenza A virus

C;Date: 21-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jul-2000

C;Accession: S09649

R;Baklemishev, A.B.; Blinov, V.M.; Vassilenko, S.K.; Golovin, S.Y.; Karginov, V.A.; Mama

Bioorg. Khim. 11, 641-645, 1985

A;Title: Synthesis, cloning and sequencing of a full-length DNA copy of the fragment 8 o

A;Reference number: S09648; MUID:85307107; PMID:4038350

A;Accession: S09649

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-121 <BEK>

A;Cross-references: EMBL:X52146; NID:G60716; PIDN:CAB38574.1; PID:G4490559

C;Genetics:

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

Query Match 94.6%; Score 574; DB 2; Length 121;  
Best Local Similarity 94.2%; Pred. No. 2.4e-42;  
Matches 114; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKMQLGSSSEDLNGIITQFESLKYRDSLGAVMRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKMQLGSSSEDLNGMITQFESLKYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGKWRQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RNEKWRQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALHLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

#### RESULT 10

MNIVXX

nonstructural protein NS2 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fr

C:Species: influenza A virus  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
C:Accession: A30086  
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.  
Virology 158, 465-468, 1987  
A:Title: Genetic divergence of the NS genes of avian influenza viruses.  
A:Reference number: A94361; MUID:87236215; PMID:2954302  
A:Accession: D27846  
A:Molecule type: genomic RNA  
A:Residues: 1-118 <NAK>  
A:Cross-references: GB:M17070; NID:g324854; PIDN:AAA43549.1; PID:g324856  
C:Genetics:  
A:Map position: segment 8  
A:Introns: 7/3  
A:Superfamily: influenza virus nonstructural protein NS2  
C:Keywords: alternative splicing; nonstructural protein

Query Match 93.7%; Score 569; DB 1; Length 118;  
Best Local Similarity 95.8%; Pred. No. 6.2e-42;  
Matches 113; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 NTVSSFDILMRISKMGSSSEDNGIITQFESLKYRDSLGAEVVRMGDLHSLQNRNG 63  
DB 1 NTVSSFDILMRISKMGSSSEDNGIITQFESLKYRDSLGAEVVRMGDLHSLQNRNG 60  
QY 64 KWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 121  
DB 61 KWREQLSQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 118

RESULT 11  
MNIV2  
nonstructural protein NS2 - influenza A virus (strain A/PR/8/34)  
C:Species: influenza A virus  
C:Date: 30-Apr-1981 #sequence\_revision 30-Apr-1981 #text\_change 16-Jul-1999  
C:Accession: A04096  
R:Baez, M.; Taussig, R.; Zazra, J.J.; Young, J.F.; Palese, P.; Reisfeld, A.; Skalka, A.M.  
Nucleic Acids Res. 8, 5845-5858, 1980  
A:Title: Complete nucleotide sequence of the influenza A/PR/8/34 virus NS gene and comparison with other influenza A virus NS genes.  
A:Reference number: A93714; MUID:81124304; PMID:7465426  
A:Accession: A04096  
A:Molecule type: genomic RNA  
A:Residues: 1-121 <BAE>  
A:Cross-references: GB:V01104; NID:g60803; PIDN:CAA24293.1; PID:g60805  
C:Genetics:  
A:Map position: segment 8  
A:Superfamily: influenza virus nonstructural protein NS2  
C:Keywords: alternative splicing

Query Match 93.4%; Score 567; DB 1; Length 121;  
Best Local Similarity 93.4%; Pred. No. 9.4e-42;  
Matches 113; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDNTVSSFDILMRISKMGSSSEDNGIITQFESLKYRDSLGAEVVRMGDLHSLQNRNG 60  
DB 1 MDNTVSSFDILMRISKMGSSSEDNGIITQFESLKYRDSLGAEVVRMGDLHSLQNRNG 60  
QY 61 RCKWTEQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 120  
DB 61 RNEKWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 120  
QY 121 I 121  
DB 121 I 121

RESULT 12  
MNIV4  
nonstructural protein NS2 - influenza A virus (strain A/Duck/England/56 [H1N6]) (fragment)  
C:Species: influenza A virus  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
C:Accession: D27846

R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.  
Virology 158, 465-468, 1987  
A:Title: Genetic divergence of the NS genes of avian influenza viruses.  
A:Reference number: A94361; MUID:87236215; PMID:2954302  
A:Accession: D27846  
A:Molecule type: genomic RNA  
A:Residues: 1-118 <NAK>  
A:Cross-references: GB:M16563; NID:g324786; PIDN:AAA43511.1; PID:g324788  
C:Genetics:  
A:Map position: segment 8  
A:Introns: 7/3  
A:Superfamily: influenza virus nonstructural protein NS2  
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.9%; Score 564; DB 1; Length 118;  
Best Local Similarity 94.9%; Pred. No. 1.7e-41;  
Matches 112; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NTVSSFDILMRISKMGSSSEDNGIITQFESLKYRDSLGAEVVRMGDLHSLQNRNG 63  
DB 1 NTVSSFDILMRISKMGSSSEDNGIITQFESLKYRDSLGAEVVRMGDLHSLQNRNG 60  
QY 64 KWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 121  
DB 61 KWREQLSQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 118

RESULT 13  
MNIV8  
nonstructural protein NS2 - influenza A virus (strain A/Duck/Ukraine/63 [H3N8]) (fragment)  
C:Species: influenza A virus  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
C:Accession: H27846  
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.  
Virology 158, 465-468, 1987  
A:Title: Genetic divergence of the NS genes of avian influenza viruses.  
A:Reference number: A94361; MUID:87236215; PMID:2954302  
A:Accession: H27846  
A:Molecule type: genomic RNA  
A:Residues: 1-118 <NAK>  
A:Cross-references: GB:M16565; NID:g324789; PIDN:AAA43513.1; PID:g324791  
C:Genetics:  
A:Map position: segment 8  
A:Introns: 7/3  
A:Superfamily: influenza virus nonstructural protein NS2  
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.9%; Score 564; DB 1; Length 118;  
Best Local Similarity 94.9%; Pred. No. 1.7e-41;  
Matches 112; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NTVSSFDILMRISKMGSSSEDNGIITQFESLKYRDSLGAEVVRMGDLHSLQNRNG 63  
DB 1 NTVSSFDILMRISKMGSSSEDNGIITQFESLKYRDSLGAEVVRMGDLHSLQNRNG 60  
QY 64 KWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 121  
DB 61 KWREQLSQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 118

RESULT 14  
MNIVB4  
nonstructural protein NS2 - influenza A virus (strain A/pintail/Alberta/119/79)  
C:Species: influenza A virus  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 08-Apr-1994  
C:Accession: H32662  
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.  
Virology 171, 1-9, 1989  
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, at  
A:Reference number: A32662; MUID:89299445; PMID:2525836  
A:Accession: H32662

A:Molecule type: genomic RNA  
A:Residues: 1-121 <TR>  
C:Genetics:  
A:Gene: NS2  
A:Map position: segment 8  
A:Introns: 10/3  
C:Superfamily: influenza virus nonstructural protein NS2  
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.9%; Score 564; DB 1; Length 121;  
Best Local Similarity 93.4%; Pred. No. 1.7e-41;  
Matches 113; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MDPNTVSSFDILMRISKQMGSSSEDLNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60  
DB 1 MDSNTVSSFDILMRISKQMGSSSEDLNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60  
QY 61 RRGKWEQQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIIRTFSPQL 120  
DB 61 RRGKWEQQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIIRTFSPQL 120  
QY 121 I 121  
DB 121 I 121

RESULT 15

nonstructural protein NS2 - influenza A virus (strains A/pintail/Alberta/268/78 and A/ma  
C:Species: influenza A virus  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 19-Oct-1995  
C:Accession: B32662; D32662  
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.  
Virology 171, 1-9, 1989  
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,  
A:Reference number: A32662; MUID:89299445; PMID:2525836  
A:Accession: B32662  
A:Molecule type: genomic RNA  
A:Residues: 1-121 <TR>  
A:Experimental source: strain A/pintail/Alberta/268/78  
A:Accession: D32662  
A:Molecule type: genomic RNA  
A:Residues: 1-121 <TR>  
A:Experimental source: strain A/mallard/New York/6750/78  
C:Genetics:  
A:Gene: NS2  
A:Map position: segment 8  
A:Introns: 10/3  
C:Superfamily: influenza virus nonstructural protein NS2  
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.8%; Score 563; DB 1; Length 121;  
Best Local Similarity 93.4%; Pred. No. 2.1e-41;  
Matches 113; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MDPNTVSSFDILMRISKQMGSSSEDLNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60  
DB 1 MDSNTVSSFDILMRISKQMGSSSEDLNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60  
QY 61 RRGKWEQQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIIRTFSPQL 120  
DB 61 RRGKWEQQLGQKPEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIIRTFSPQL 120  
QY 121 I 121  
DB 121 I 121

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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:32:32 ; Search time 75.4957 Seconds  
(without alignments)  
820.730 Million cell updates/sec

Title: US-10-654-737-6

Perfect score: 607

Sequence: 1 MDPNTVSSFDILMRISKMQ.....ALQLLLEVEQEIRTFSQLI 121

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	604	99.5	121	2 Q89733	Q89733 influenza a
2	600	98.8	121	2 Q67248	Q67248 influenza a
3	597	98.4	121	1 VNS2 IAUSS	P03504 influenza a
4	596	98.2	121	2 Q06049	Q06049 influenza a
5	594	97.9	121	1 VNS2 IAANN	P21432 influenza a
6	594	97.9	121	2 Q6XTJ1	Q6xtj1 influenza a
7	594	97.9	121	2 Q6XTJ7	Q6xtj7 influenza a
8	590	97.2	121	1 VNS2 IALB2	P26133 influenza a
9	590	97.2	121	2 Q67264	Q67264 influenza a
10	590	97.2	121	2 Q6XTI9	Q6xti9 influenza a
11	590	97.2	121	2 Q6XTI5	Q6xti5 influenza a
12	589	97.0	121	2 Q8QIT5	Q8qlt5 influenza a
13	589	97.0	121	2 Q6XTI5	Q6xti5 influenza a
14	589	97.0	121	2 Q6XTI7	Q6xti7 influenza a
15	588	96.9	121	1 VNS2 IAFOM	P03506 influenza a
16	587	96.7	121	1 VNS2 IACHI	P11619 influenza a
17	587	96.7	121	2 Q67255	Q67255 influenza a
18	587	96.7	121	2 Q6XTJ5	Q6xtj5 influenza a
19	587	96.7	121	2 Q771X1	Q771x1 influenza a
20	586	96.5	121	1 VNS2 IAFOW	P03505 influenza a
21	586	96.5	121	2 Q693C3	Q693c3 influenza a
22	586	96.5	121	2 Q6DQJ2	Q6dqj2 influenza a
23	586	96.5	121	2 Q6DSV1	Q6dsv1 influenza a
24	586	96.5	121	2 Q612B7	Q612b7 influenza a
25	586	96.5	121	2 Q6XTC3	Q6xtc3 influenza a
26	586	96.5	121	2 Q6XTF1	Q6xtf1 influenza a
27	586	96.5	121	2 Q6XTF3	Q6xtf3 influenza a
28	586	96.5	121	2 Q6XTF5	Q6xtf5 influenza a
29	586	96.5	121	2 Q6XTF7	Q6xtf7 influenza a
30	586	96.5	121	2 Q6XTF9	Q6xtf9 influenza a
31	586	96.5	121	2 Q6XTG1	Q6xtg1 influenza a

32	586	96.5	121	2 Q6XTG3	Q6xtg3 influenza a
33	586	96.5	121	2 Q6XTG5	Q6xtg5 influenza a
34	586	96.5	121	2 Q6XTG9	Q6xtg9 influenza a
35	586	96.5	121	2 Q6XTH1	Q6xth1 influenza a
36	586	96.5	121	2 Q6XTH7	Q6xth7 influenza a
37	586	96.5	121	2 Q6XTH9	Q6xth9 influenza a
38	586	96.5	121	2 Q6XTI1	Q6xti1 influenza a
39	586	96.5	121	2 Q77AL4	Q77al4 influenza a
40	585	96.4	121	2 Q8QLS0	Q8qls0 influenza a
41	584	96.4	121	2 Q41648	Q41648 influenza a
42	584	96.2	121	2 Q6XTJ3	Q6xtj3 influenza a
43	584	96.2	121	2 Q6XTJ9	Q6xtj9 influenza a
44	583	96.0	121	1 VNS2 IAPI0	P13148 influenza a
45	583	96.0	121	2 Q6XTG7	Q6xtg7 influenza a

#### ALIGNMENTS

RESULT 1  
Q89733 PRELIMINARY; PRT; 121 AA.  
ID Q89733  
AC Q89733;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE Non-structural protein 2.  
GN Names=NS2;  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenzavirus A.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/WS/33; TISSUE=Embryonated;  
RA Husak P.J.;  
RL Thesis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert Wood Johnson Medical School.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/WSN/40; TISSUE=Mouse;  
RA Husak P.J., Schlesinger R.W.;  
RT "Replication of neurovirulent and non-neurovirulent human H1N1 influenza A viruses in mouse brain and nerve cell cultures: virus strain-specific and host cell-dependent variations in progeny virus asse.";  
RL Thesis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert Wood Johnson Medical School.  
DR EMBL; U13683; AAA21583.1; -.  
DR EMBL; U13682; AAA21581.1; -.  
DR InterPro; IPR000968; Flu NS2.  
DR Pfam; PF00601; Flu NS2; 1.  
SQ SEQUENCE 121 AA; 14327 MW; B15C14C594F55922 CRC64;

Query Match 99.5%; Score 604; DB 2; Length 121;

Best Local Similarity 99.2%; Pred. No. 5.7e-44;

Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDPNTVSSFDILMRISKMQSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN	60
Db	1	MDPNTVSSFDILMRISKMQSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN	60
Qy	61	RNGKVRQEQGQKFEIRWLIEVRHLKKTENSFEQITFMQALQLLLEVEQEIRTFSQL	120
Db	61	RNGKVRQEQGQKFEIRWLIEVRHLKKTENSFEQITFMQALQLLLEVEQEIRTFSQL	120
Qy	121	I 121	
Db	121	I 121	

RESULT 2  
Q67248

```

ID Q67248 PRELIMINARY; PRT; 121 AA.
AC Q67248;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Nonstructural protein.
GN Name=NS2;
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96082767; PubMed=7483294;
RA Ward A.C., Azad A.A., McKimm-Breschkin J.L.;
RT "Changes in the NS gene of neurovirulent strains of influenza affect
RT splicing.";
RL Virus Genes 10:91-94(1995).
DR EMBL; L25720; AAA91329.1; --
DR PDB; 1PD3; X-ray; A/B=59-116.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2; I.
KW Nonstructural protein.
SQ SEQUENCE 121 AA; 14326 MW; B15C197E22F8E294 CRC64;

Query Match 98.8%; Score 600; DB 2; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.3e-43;
Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQPESLKYRDSLGEAVNRMGDLHSLQN 60
DB 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQPESLKYRDSLGEAVNRMGDLHSLQN 60
QY 61 RKGKWEQLGQKPEIRWLIEEVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB 61 RKGKWEQLGQKPEIRWLIEEVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
QY 121 I 121
DB 121 I 121

RESULT 3
VNS2_IAUSS STANDARD; PRT; 121 AA.
AC P03504;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural protein NS2.
GN Name=NS; Synonyms=8;
OS Influenza A virus (strain A/USSR/90/77 H1N1).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=225083;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164298; PubMed=6834468;
RA Krystal M., Buonagurio D.A., Young J.F., Palese P.;
RT "Sequential mutations in the NS genes of influenza virus field
RT strains.";
RL J. Virol. 45:547-554(1983).
CC -I- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NS2;
CC IsoId=P03504-1; Sequence=Displayed;
CC Name=NS1;
CC IsoId=P03498-1; Sequence=External;
CC -----
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CC -----
DR EMBL; K00578; AAA43539.1; --
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2; I.
KW Alternative splicing; Nonstructural protein.
SQ SEQUENCE 121 AA; 14379 MW; DB9C108190B51584 CRC64;

Query Match 98.4%; Score 597; DB 1; Length 121;
Best Local Similarity 97.5%; Pred. No. 2.3e-43;
Matches 118; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQPESLKYRDSLGEAVNRMGDLHSLQN 60
DB 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQPESLKYRDSLGEAVNRMGDLHSLQN 60
QY 61 RKGKWEQLGQKPEIRWLIEEVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB 61 RKGKWEQLGQKPEIRWLIEEVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
QY 121 I 121
DB 121 I 121

RESULT 4
Q60649 PRELIMINARY; PRT; 121 AA.
ID Q60649;
AC Q60649;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Non-structural protein 1.
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93275765; PubMed=8502573;
RA Ward A.C., Azad A.A., Macreadie I.G., McKimm-Breschkin J.L.;
RT "Complete nucleotide sequence of the non-structural gene of the human
RT influenza virus strain A/WS/33.";
RL Nucleic Acids Res. 21:2257-2257(1993).
DR EMBL; Z21498; CAA79707.1; --
DR PIR; S33685; S33685.
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2; I.
SQ SEQUENCE 121 AA; 14399 MW; B15C16C794F75B22 CRC64;

Query Match 98.2%; Score 596; DB 2; Length 121;
Best Local Similarity 98.3%; Pred. No. 2.8e-43;
Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQPESLKYRDSLGEAVNRMGDLHSLQN 60
DB 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQPESLKYRDSLGEAVNRMGDLHSLQN 60
QY 61 RKGKWEQLGQKPEIRWLIEEVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB 61 RKGKWEQLGQKPEIRWLIEEVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
QY 121 I 121
DB 121 I 121

RESULT 5
VNS2_IAANN STANDARD; PRT; 121 AA.
ID VNS2_IAANN

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AC P21432;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural protein NS2.
GN Names=8;
OS Influenza A virus (strain A/Ann Arbor/6/60), and
OC Influenza A virus (strain A/Leningrad/134/57 H2N2).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OC NCBI_TaxID=135322, 128148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Ann Arbor/6/60;
RX MEDLINE=69073759; PubMed=2974219;
RA Cox N.J., Kitame F., Kendal A.P., Maassab H.F., Naeye C.; live
RT "Identification of sequence changes in the cold-adapted, live
RL attenuated influenza vaccine strain, A/Ann Arbor/6/60 (H2N2).";
RL Virology 167:554-567(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Leningrad/134/57;
RX MEDLINE=92124758; PubMed=1733114;
RA Klimov A.I., Cox N.J., Yotov W.V., Rocha E., Alexandrova G.I.,
RA Kendal A.P.;
RT "Sequence changes in the live attenuated, cold-adapted variants of
RT Influenza A/Leningrad/134/57 (H2N2) virus.";
RL Virology 186:795-797(1992).
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NS2;
CC IsoId=P21432-1; Sequence=Displayed;
CC Name=NS1;
CC IsoId=P21431-1, P26131-1;
CC Sequence=External;
CC -----
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CC -----
DR EMBL; M23968; AAA43552.1; -
DR EMBL; M81572; AAA19198.1; -
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2.1.
KW Alternative splicing; Nonstructural protein.
SQ SEQUENCE 121 AA; 14351 MW; DB9C1097D2D12584 CRC64;

Query Match 97.9%; Score 594; DB 1; Length 121;
Best Local Similarity 96.7%; Pred. No. 4.1e-43;
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
QY 61 RKGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RKGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
QY 121 I 121
DB 121 I 121

RESULT 6
Q6XTJ1 PRELIMINARY; PRT; 121 AA.
ID Q6XTJ1
AC Q6XTJ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
US-10-654-737-6.rup
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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS2.
OS Influenza A virus (A/Malaya/16/58 (H2N2)).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OC NCBI_TaxID=220954;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210156; AAC46578.1; -
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2.1.
SQ SEQUENCE 121 AA; 14351 MW; DB9C1097D2D12584 CRC64;

Query Match 97.9%; Score 594; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 4.1e-43;
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
QY 61 RKGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RKGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
QY 121 I 121
DB 121 I 121

RESULT 7
Q6XTJ7 PRELIMINARY; PRT; 121 AA.
ID Q6XTJ7
AC Q6XTJ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Non-structural protein NS2.
OS Influenza A virus (A/Davis/1/57 (H2N2)).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OC NCBI_TaxID=220951;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210153; AAC46572.1; -
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2.1.
SQ SEQUENCE 121 AA; 14351 MW; DB9C1097D2D12584 CRC64;

Query Match 97.9%; Score 594; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 4.1e-43;
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
QY 61 RKGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RKGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSQL 120
QY 121 I 121
DB 121 I 121

RESULT 8
VNS2_TALE2
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ID VNS2_IABE2 STANDARD; PRT; 121 AA.
AC P26133;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nonstructural protein NS2.
GN Name=8;
OS Influenza A virus (strain A/Leningrad/134/17/57 H2N2), and
OS Influenza A virus (strain A/Leningrad/134/47/57 H2N2).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=152281; 152282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124758; PubMed=1733114;
RA Klimov A.I., Cox N.J., Yotov W.V., Rocha E., Alexandrova G.I.,
RA Kendal A.P.;
RT "Sequence changes in the live attenuated, cold-adapted variants of
RT influenza A/Leningrad/134/57 (H2N2) virus.";
RL Virology 186:795-797(1992).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NS2;
CC IsoId=P26133-1; Sequence=Displayed;
CC Name=NS1;
CC IsoId=P26131-1; Sequence=External;
CC -----
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DR EMBL; M81578; AA19200.1; -.
DR EMBL; M81584; AA19202.1; -.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
KW Alternative splicing; Nonstructural protein.
SQ SEQUENCE 121 AA; 14333 MW; DB9C1097D2D64844 CRC64;

Query Match 97.2%; Score 590; DB 1; Length 121;
Best Local Similarity 95.9%; Pred. No. 9e-43;
Matches 116; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESKLKLYRDSLGEAVMRMGDLHSLQN 60
DB 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESKLKLYRDSLGEAVMRMGDLHSLQN 60

QY 61 RKGKWEQLGQKFEIRWLIEVVRHLKLTENSFEQITFMQALQLLLEVEQEIRTFSFOL 120
DB 61 RKGKWEQLGQKFEIRWLIEVVRHLKLTENSFEQITFMQALQLLLEVEQEIRTFSFOL 120

QY 121 I 121
DB 121 I 121

RESULT 9
Q67264 PRELIMINARY; PRT; 121 AA.
ID Q67264;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE Nonstructural protein 2.
GN Name=NS2;
OS Influenza A virus.
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124758; PubMed=2053297;
RA Schultz U., Fitch W.M., Ludwig S., Mandler J., Scholtissek C.;
RA "Evolution of pig influenza viruses.";
RL Virology 183:61-73(1991).
DR EMBL; M55484; AA43498.1; -.
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00600; Flu NS1; 1.
DR Pfam; PF00601; Flu NS2; 1.
KW Nonstructural protein.
SQ SEQUENCE 121 AA; 14349 MW; F47E29D7D471C6F CRC64;

Query Match 97.2%; Score 590; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 9e-43;
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESKLKLYRDSLGEAVMRMGDLHSLQN 60
DB 1 MDSNTVSSFDILMRISKVQLGSSSEDNGIITQFESKLKLYRDSLGEALMRMGDLHSLQN 60

QY 61 RKGKWEQLGQKFEIRWLIEVVRHLKLTENSFEQITFMQALQLLLEVEQEIRTFSFOL 120
DB 61 RKGKWEQLGQKFEIRWLIEVVRHLKLTENSFEQITFMQALQLLLEVEQEIRTFSFOL 120

QY 121 I 121
DB 121 I 121

RESULT 10
Q6XTI9 PRELIMINARY; PRT; 121 AA.
ID Q6XTI9;
AC Q6XTI9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Non-structural protein NS2.
OS Influenza A virus (A/Albany/6/58 (H2N2)).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220953;
RN [1]
RP SEQUENCE FROM N.A.
RX Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210157; AA046580.1; -.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
SQ SEQUENCE 121 AA; 14350 MW; DB9C1D2C64DC9E32 CRC64;

Query Match 97.2%; Score 590; DB 2; Length 121;
Best Local Similarity 95.9%; Pred. No. 9e-43;
Matches 116; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESKLKLYRDSLGEAVMRMGDLHSLQN 60
DB 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESKLKLYRDSLGEAVMRMGDLHSLQN 60

QY 61 RKGKWEQLGQKFEIRWLIEVVRHLKLTENSFEQITFMQALQLLLEVEQEIRTFSFOL 120
DB 61 RKGKWEQLGQKFEIRWLIEVVRHLKLTENSFEQITFMQALQLLLEVEQEIRTFSFOL 120

QY 121 I 121
DB 121 I 121

RESULT 11
Q6XTKI PRELIMINARY; PRT; 121 AA.
ID Q6XTKI
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AC Q6XTK1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS2.
OS Influenza A virus (strain A/Singapore/1/57 H2N2).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220949;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E.; Cox N.J.; Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210151; AAC46584.1; -.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
SQ SEQUENCE 121 AA; 14381 MW; DB8C0196C2C02484 CRC64;

Query Match 97.2%; Score 590; DB 2; Length 121;
Best Local Similarity 95.9%; Pred. No. 9e-43; Mismatches 2; Indels 0; Gaps 0;
Matches 116; Conservative 3;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60
DB 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

QY 61 RKGKREQLGQKFEIRWLIEVRHLKITENSFEQITFMQALQLLLEVEQIRTFSQL 120
DB 61 RKGKREQLGQKFEIRWLIEVRHLKITENSFEQITFMQALQLLLEVEQIRTFSQL 120

QY 121 I 121
DB 121 I 121

RESULT 12
Q8QLT5 PRELIMINARY; PRT; 121 AA.
AC Q8QLT5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Non structural protein 2.
GN Name=NS2;
OS Influenza A virus (A/Swine/Cote d'Armor/3633/84 (H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
OX NCBI_TaxID=164041;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-A/swine/Cotes d'Armor/3633/84;
RX MEDLINE=21904432; PubMed=11907321;
RA Marozin S.; Gregory V.; Cameron K.; Bennett M.; Valette M.; Aymard M.;
RA Poni E.; Barigazzi G.; Lin Y.; Hay A.;
RT "Antigenic and genetic diversity among swine influenza A H1N1 and H1N2 viruses in Europe.";
RL J. Gen. Virol. 83:735-745 (2002).
DR EMBL; AJ344025; CAC86628.1; -.
DR GO; GO:0003723; rRNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00600; Flu NS1; 1.
DR Pfam; PF00601; Flu NS2; 1.
SQ SEQUENCE 121 AA; 14330 MW; 149A445351AD7865 CRC64;

Query Match 97.0%; Score 589; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 1.1e-42; Mismatches 1; Indels 0; Gaps 0;
Matches 117; Conservative 3;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60
DB 1 MDSNTVSSFDILMRISKVQLGSSSKDNGIITQFESLKYRDSLGEALRMGDLHSLQN 60

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QY 61 RKGKREQLGQKFEIRWLIEVRHLKITENSFEQITFMQALQLLLEVEQIRTFSQL 120
DB 61 RKGKREQLGQKFEIRWLIEVRHLKITENSFEQITFMQALQLLLEVEQIRTFSQL 120

QY 121 I 121
DB 121 I 121

RESULT 13
Q6XTI5 PRELIMINARY; PRT; 121 AA.
AC Q6XTI5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS2.
OS Influenza A virus (A/SaoPaolo/3/59 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E.; Cox N.J.; Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210159; AAC46584.1; -.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
SQ SEQUENCE 121 AA; 14339 MW; CB721B67D2D12584 CRC64;

Query Match 97.0%; Score 589; DB 2; Length 121;
Best Local Similarity 95.9%; Pred. No. 1.1e-42; Mismatches 2; Indels 0; Gaps 0;
Matches 116; Conservative 3;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60
DB 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

QY 61 RKGKREQLGQKFEIRWLIEVRHLKITENSFEQITFMQALQLLLEVEQIRTFSQL 120
DB 61 RKGKREQLGQKFEIRWLIEVRHLKITENSFEQITFMQALQLLLEVEQIRTFSQL 120

QY 121 I 121
DB 121 I 121

RESULT 14
Q6XTI7 PRELIMINARY; PRT; 121 AA.
AC Q6XTI7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS2.
OS Influenza A virus (A/Victoria/15681/59 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220956;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E.; Cox N.J.; Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210159; AAC46582.1; -.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
SQ SEQUENCE 121 AA; 14339 MW; CB721B67D2D12584 CRC64;

Query Match 97.0%; Score 589; DB 2; Length 121;
Best Local Similarity 95.9%; Pred. No. 1.1e-42; Mismatches 2; Indels 0; Gaps 0;
Matches 116; Conservative 3;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

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Db 1 MDPNTVSSFDILMRKSKMQLGSSSEDLNGMITQFESLKYRDSLGEAVVRMGDLHSLQN 60
QY 61 RRGKWEQQLGQKFEERWLIEEVRRHLKKTENSFEQITFMQALQLLLEVEQEIRTFSPQL 120
Db 61 RRGKWEQQLGQKFEERWLIEEVRRHLKKTENSFEQITFMQALQLLLEVEQEIRTFSPQL 120
QY 121 I 121
Db 121 I 121

RESULT 15
VNS2 IAFOM STANDARD; PRT; 121 AA.
AC P03506;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nonstructural protein NS2.
GN Name=8;
OS Influenza A virus (strain A/Fort Monmouth/1/47 H1N1).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=229411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164298; PubMed=6834468;
RA Krystal M.; Buonagurio D.A.; Young J.F.; Palese P.;
RT "Sequential mutations in the NS genes of influenza virus field strains.";
RL J. Virol. 45:547-554(1983).
CC -!- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NS2;
CC IsoId=P03506-1; Sequence=Displayed;
CC Name=NS1;
CC IsoId=P03499-1; Sequence=External;
CC -----
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CC -----
DR EMBL; K00576; AAA43524.1; -;
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
KW Alternative splicing; Nonstructural protein.
SQ SEQUENCE 121 AA; 14300 MW; ED67C64D21C9BE9F CRC64;

Query Match 96.9%; Score 588; DB 1; Length 121;
Best Local Similarity 95.9%; Pred. No. 1.3e-42;
Matches 116; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRKSKMQLGSSSEDLNGITQFESLKYRDSLGEAVVRMGDLHSLQN 60
Db 1 MDPNTVSSFDILMRKSKMQLGSSSEDLNGVITLFESLKYRDSLGEAVVRMGDLHSLQN 60
QY 61 RRGKWEQQLGQKFEERWLIEEVRRHLKKTENSFEQITFMQALQLLLEVEQEIRTFSPQL 120
Db 61 RRGKWEQQLGQKFEERWLIEEVRRHLKKTENSFEQITFMQALQLLLEVEQEIRTFSPQL 120
QY 121 I 121
Db 121 I 121
```